STUDIES ON WHEAT RESISTANCE TO UG99

A DISSERTATION
SUBMITTED TO THE FACULTY OF THE GRADUATE SCHOOL
OF THE UNIVERSITY OF MINNESOTA
BY

MATTHEW NOLAN ROUSE

IN PARTIAL FULFILLMENT OF THE REQUIREMENTS
FOR THE DEGREE OF
DOCTOR OF PHILOSOPHY

YUE JIN

OCTOBER 2010

Acknowledgements

The research completed was facilitated by the gracious help from several people at the University of Minnesota department of Agronomy and Plant Genetics and department of Plant Pathology (St. Paul, Minnesota), the USDA-ARS Cereal Disease Laboratory (St. Paul, Minnesota), and the USDA-ARS Cereal Crops Research (Fargo, North Dakota). Lucy Wanschura, Sam Gale, and Pablo Olivera taught me many of the techniques in working with stem rust. Sixin Liu and Jen Flor taught me how to run acrylamide gels and helped in trouble shooting experimental hurdles. Mary Osenga taught me how to use pipetting robots and a capillary electrophoresis system. Several undergraduate student technicians contributed to extracting DNA and managing plants in the greenhouses including Trish Weitemier, Gael Zembal, Jesse Rouse, Randi Staudinger, and Sarah Nelson. Brian Steffenson provided use of the resources available in his lab and advice on constructing experiments. Jim Anderson and Shiaoman Chao allowed me to work in their labs and directed me to appropriate experimental strategies. Les Szabo, Marty Carson and Jim Kolmer served on the graduate committee at various capacities. Field screening in Njoro Kenya would not be possible without coordination and assistance from Peter Njau and Ruth Wanyera of the Kenya Agricultural Research Institute. Bob McIntosh provided insight into the reaction of *Sr21* to TTKSK and into *Triticum monococcum* gene postulations. Harold Bockelman, USDA-ARS, National Small Grains Collection, Aberdeen Idaho, distributed seed of *T. monococcum*, *T. urartu*, *T. aestivum*, and *Aegilops tauschii* accessions. Colin Heibert, Agriculture and Agri-Food,

Canada, provided seed of RL5288 and RL5289. Mike Pumphrey provided *Aegilops tauschii* seed from the Wheat Genetics and Genomics Resources Center, Manhattan, Kansas. Eric Olson, department of Plant Pathology, Kansas State University, Manhattan, Kansas, screened *A. tauschii* accessions with races RKQQC, QTHJC, and TPMKC. Funding to support my graduate education was provided by the USDA-ARS and USAID through the department of Plant Pathology and the department of Agronomy and Plant Genetics at the University of Minnesota. Funding for research was provided by USDA-ARS, USAID, and the Bill and Melinda Gates Foundation. Bob Bowden, USDA-ARS, Manhattan, Kansas, inspired me to pursue studying wheat resistance to rust. Most of all, I would like to acknowledge and thank my advisor, Yue Jin, for his direction, guidance, training, dedication, reproof, and leadership during the last three years.

Dedication

This dissertation is dedicated to Norman Borlaug (1914-2009). Borlaug's dedication to wheat breeding for the alleviation of poverty and starvation and his persistence in convincing public policy makers to adopt agricultural technologies such as high-yielding, disease-resistant wheat are epic and inspirational contributions to the world.

Abstract

Wheat stem rust caused by the fungus *Puccinia graminis* f. sp. *tritici* (*Pgt*) has historically been a devastating disease of wheat. In 1998, a race of *Pgt* was detected in Uganda that is virulent to the majority of wheat cultivars being grown. This new race, commonly referred to as Ug99, was characterized as race TTKSK based upon the North American stem rust differentials. Race TTKSK has recently spread throughout eastern and southern Africa, and into the Middle East. Data suggest that Ug99 can alternatively be described as *Pgt* race PTKSK, based upon demonstrated avirulence to stem rust resistance gene *Sr21*. Accessions of wild relatives of wheat, *Triticum monococcum*, *T. urartu*, and *Aegilops tauschii* were screened with *Pgt* race TTKSK. Crosses among resistant and susceptible accessions of *T. monococcum* led to the characterization of two new stem rust resistance genes effective to *Pgt*-TTKSK. Preliminary screening of 700 accessions of spring wheat led to the identification of 88 accessions with resistance to Ug99. Examination of the genetics of resistance in one of these accessions, SD 1691, identified *Sr28* as conferring a high level of resistance. Molecular markers linked to *Sr28* were identified on chromosome arm 2BL. Examination of the genetics of resistance in Gabo 56 indicated the presence of a single dominant gene. This gene was temporarily designated as *SrGabo56* and mapped on chromosome arm 2BL. Segregation of resistance in the progeny of the cross between SD 1691 and Gabo 56 indicated that *Sr28* and *SrGabo56* are linked. Characterization of the genetics of resistance to *Pgt*-TTKSK in synthetic wheat TA4152-37, resulted in the identification of *Sr13* in TA4152-37.

Molecular markers linked to *Sr13* in hexaploid wheat were identified on chromosome arm 6AL. Overall, 3 new stem rust resistance genes effective to *Pgt*-TTKSK were identified. Molecular markers linked to *SrGabo56*, *Sr13*, and *Sr28* were described. The identification of markers linked to multiple stem rust resistance genes will facilitate the combination of these genes in breeding lines. The identification of the new sources of resistance to *Pgt*-TTKSK will provide plant breeders with additional tools to protect wheat from this dangerous race.

Table of Contents

List of Tables

List of Figures

Forward

The chapters of this dissertation were written and formatted for publication individually in specific scientific journals. Any redundancies of information or inconsistencies in formatting result from this publication plan.

Chapter I

Literature Review

Wheat stem rust, caused by the basidiomycete fungus *Puccinia graminis* f. sp. *tritici* (Eriks. & E. Henn.; *Pgt*), has been effectively controlled worldwide largely through the deployment of resistant varieties of wheat. In 1998, a race of *Pgt* was identified in Uganda that was shown to be (1) the first race with virulence to stem rust resistance gene *Sr31* and (2) virulent on the majority of widely deployed resistance genes (Pretorius et al., 2000; Jin et al., 2007). This *Pgt* isolate was classified as race TTKSK according to the North American differential set (Roelfs and Martens, 1988; Wanyera et al., 2006; Jin et al., 2008) and is commonly known as Ug99. The race drew international attention when Norman Borlaug visited Kenya in 2004, saw the epidemic of wheat stem rust caused by *Pgt*-TTKSK, and voiced the threat that this race poses for the global wheat crop.

In 2006, isolates of *Pgt* were detected in Kenya that caused a high seedling infection-type on lines with resistance gene *Sr24* (Jin et al., 2008). This variant was designated as *Pgt* race TTKST, a variant of Ug99 with additional virulence on *Sr24*. Race TTKST came to predominate the stem rust population in Kenya in 2007. Also in 2006, isolates of *Pgt*-TTKSK were characterized from Yemen indicating that Ug99 had migrated out of Africa (Singh et al., 2008).

In 2007, isolates of *Pgt* were identified in Kenya from susceptible pustules on adult plants carrying resistance gene *Sr36*. These isolates were confirmed to be yet another variant of Ug99 designated as race TTTSK (Jin et al., 2009). The same year, Ug99 had been confirmed to infect wheat in Iran (Nazari et al., 2009). This migration brings Ug99 closer to the intensive wheat production area in the Indo-Gangetic plain.

In 2009, isolates of *Pgt* were detected in South Africa with virulence to *Sr31* (Pretorius et al., 2010). Race analysis identified these isolates as race PTKST with virulence to *Sr24* and *Sr31*, but with avirulence to *Sr21*. Previous race analysis experiments described races very similar to *Pgt*-TTKSK in South Africa except for avirulence to *Sr21* and *Sr31* (Visser et al., 2009). Based upon analysis of the literature, isolates of the *Pgt*-TTKSK complex can be differentiated by stem rust resistance genes *Sr21*, *Sr24*, *Sr31*, and *Sr36*. However, confirmation is needed to verify that isolates of the *Pgt*-TTKSK complex exist with variable reactions to *Sr21*.

This detection of variants of Ug99 with virulence on *Sr24* and *Sr36* is significant because of the predominance of these genes in wheat cultivars that are classified as resistant to *Pgt*-TTKSK. Jin and Singh (2006) screened 450 cultivars and advanced breeding lines from the Unites States and found the majority of resistant lines in the hard red winter wheat class to carry *Sr24* and the majority of resistant lines in the soft red winter wheat class to carry *Sr36*. In United States wheat cultivars, two genes remaining resistant to all variants of Ug99 are *SrTmp* and a resistance gene on the 1AL.1RS wheat-rye translocation in cultivar Amigo designated as *1RS-Am*. Several races in the United States possess virulence to *SrTmp* including race MCCFC (race 56) and race TPMKC (race 15B), which caused epidemics in the 1950s. Gene *SrTmp* remains in some varieties of the current hard red winter wheat market class likely due to the widespread utilization of its donor variety, 'Triumph 64', in providing early maturing and other adaptive traits to this germplasm. Translocation *1RS-Am* resistance is effective to all North American races

tested, but virulence has been found in Ethiopia and Yemen conferred by *Pgt* race TRTTF. This race possesses unusual virulence to *Sr13* as well.

Methods to control *Pgt*-TTKSK are needed. Fungicides have been shown to be effective against *Pgt*-TTKSK (Wanyera et al., 2009). However, plant resistance is the most economical form of control of stem rust. The effectiveness of plant resistance to rusts has often been limited to short periods of time due to changes in pathogen populations. Durable resistance is resistance that has been deployed over a large area, over a long period of time, in an environment conducive for disease, and that has remained effective (Johnson, 1984). Though resistance can only be determined to be durable in retrospect, several strategies have been proposed to breed for resistance that will be durable.

Resistance genes that recognize pathogen effector proteins that are costly for the pathogen to delete or mutate have been proposed to be more durable (Leach et al., 2001). This concept is best demonstrated in bacterial blight of rice where isolates of *Xanthomonas oryzae* pv. *oryzae* virulent on resistance gene *Xa7* were dramatically less fit than avirulent isolates (Bai et al., 2000). Unfortunately, some virulent isolates of *Pgt* have not exhibited significant fitness costs as demonstrated by their ability to cause epidemics (*Pgt* race TPMKC in the 1950's and *Pgt* race TTKSK in the 2000's).

A second strategy to obtain durable resistance is the use of horizontal resistance. Horizontal resistance is resistance that is effective against all races of the pathogen (race non-specific, general resistance) (Van Der Planck, 1968). Horizontal resistance has been used synonymously with slow rusting resistance, minor-gene resistance, partial

resistance, polygenic resistance, adult-plant resistance, additive resistance, durable resistance, and quantitative resistance, though none of these types of resistance are necessarily horizontal resistance and horizontal resistance may not be any of these aforementioned types of resistance. Wheat breeders have previously selected for cultivars with horizontal resistance to leaf and stripe rust (Singh et al., 2005). Several breeding lines with seedling susceptibility and adult-plant resistance to *Pgt*-TTKSK have been identified (Njau et al., 2010). Crosses between adapted high-yielding cultivars and lines proposed to possess horizontal resistance to *Pgt* are being made by International Maize and Wheat Improvement Center (CIMMYT) scientists in order to breed for resistance to Ug99 (Singh et al., 2006, Sing et al., 2008). A major difficulty in obtaining horizontal resistance in advanced breeding lines is the effort needed to introgress the multiple loci conferring resistance simultaneously. In order to breed for horizontal resistance, varieties that are susceptible at the seedling stage and partially resistant at the adult plant stage to all races of *Pgt* tested are crossed in order to derive progeny with an increased level of resistance. This strategy was utilized by Knott to develop lines resistant to stem rust (1988). However, 17 of 20 of these lines did not confer resistance when grown in international nurseries and exposed to diverse races of *Pgt* (Knott, 1982; Knott, 1988). Knott examined the genetics of adult plant resistance in several of these lines, selected to be susceptible at the seedling stage (1982). The exact number of adult plant genes segregating could not be estimated due to the low resolution of the populations (F_2 adult plants were phenotyped). However, Knott (1982) came to the general conclusion: "Of over 3,000 F_2 plants from 22 crosses, none was as resistant as its resistant parent line, and

in most crosses none was even close. Thus, the results indicate that resistance is controlled by a number of genes with small, cumulative effects." In summary, though the inheritance of this resistance appeared to be complex, it was also demonstrated to be largely specific to North American isolates. Researchers using a similar strategy to breed for horizontal resistance or "durable" resistance should take caution to make sure that their partially resistant parent lines are effective to diverse races of rust pathogens.

A third strategy to obtain durable resistance is the use of resistance gene pyramids. The long-term control of *Pgt* in the United States and Canada has been attributed to the deployment of resistance gene pyramids (Mundt, 1990; Kolmer et al., 1991; Mundt 1991). Combined resistance genes may provide at least three functions: (1) conferring resistance to multiple races, (2) decreasing the frequency of virulent isolates in a population and (3) increasing the probability that one of the genes in the cultivar or a specific combination of genes in the pyramid are inherently durable (isolates virulent on such genes or combinations of genes would have a significant fitness cost similar to *Xa7*). Schafer and Roelfs (1985) estimated that the frequency of a virulent isolate to six resistance genes derived from an avirulent population is 3.4×10^{-23}. Ideally, a resistance gene pyramid uses genes that (1) are not deployed singly and (2) are resistant to all races of the pathogen. Pressures to release resistant germplasm immediately after they have been discovered have led to the limited availability of resistance genes that are resistant to all races but not deployed singly. Molecular markers can be used to pyramid multiple resistance genes. Discipline will be needed to not dilute resistance gene pyramids in breeding programs.

In order to facilitate the deployment of durable resistance, additional sources of resistance to Ug99 need to be identified. Molecular markers linked to resistance genes *Sr2*, *Sr24*, *Sr25*, *Sr26*, *Sr36*, *Sr40*, and *Sr1A.1R* have been developed (These resistance genes are effective to *Pgt* race TTKSK; Liu et al., 2010; Olson et al., 2010; Tsilo et al., 2008; Yu et al., 2010). Markers linked to additional known *Sr* genes and new *Sr* genes need to be developed in order to aid breeders in selecting for resistant breeding lines and in potentially pyramiding these sources of resistance.

Recent studies suggest that the diverse *Pgt* races exist in both North America and Ethiopia (Admassu et al., 2009; Rouse et al., 2009). Continued monitoring of *Pgt* is needed in order to detect virulent races before they become widespread and an imminent threat to wheat production.

Chapter II

Sr21 mediates temperature-sensitive resistance to race TTKSK of *Puccinia graminis* f. sp. *tritici*

Summary

Isolates of *Puccinia graminis* f. sp. *tritici* (*Pgt*), the causal agent of wheat stem rust, are characterized as races based upon the disease reaction to differential monogenic wheat lines. *Pgt* race TTKSK (*Pgt*-TTKSK) has previously been classified as conditioning a high reaction on monogenic lines with stem rust resistance gene *Sr21*. However, sometimes low reactions to *Sr21* are observed when screening with *Pgt*-TTKSK and *Pgt*-TTKSK-related isolates. In order to resolve whether or not *Sr21* conditions resistance to *Pgt*-TTKSK, we screened 4 monogenic lines with *Sr21* and 4 susceptible controls with 4 isolates of the *Pgt*-TTKSK race-complex and 11 other isolates. Seedling plants were screened in growth chambers at 3 different temperatures and 3 different photoperiods in order to test the hypothesis that differences in temperature and light mediate the variable reaction of lines with *Sr21* to *Pgt*-TTKSK. We observed that temperature influenced the interaction between monogenic lines with *Sr21* and *Pgt*-TTKSK. This result is significant for global monitoring of the presence of *Pgt*-TTKSK, as race analysis of isolates classified as TTKSK, or high on *Sr21*, in one environment or replication could be classified as PTKSK, or low on *Sr21*, in another.

Introduction

Puccinia graminis f. sp. *tritici* (*Pgt*), the causal agent of wheat stem rust, has historically caused significant yield losses worldwide. In the past several decades, farmers and scientists have controlled stem rust through the use of genetic resistance, eliminating the alternate host of *Pgt* in some areas, and monitoring the pathogen population for potentially dangerous races. Monitoring the population of *Pgt* allows breeders and scientists to develop resistant varieties to virulent races of *Pgt* faster and potentially before the spread of virulent races to local wheat growing regions.

In 1999, an isolate of *Pgt* was reported in Uganda that was virulent on the majority of wheat resistance genes deployed in agriculture (Pretorius et al., 2000). This isolate was classified as race TTKSK (*Pgt*-TTKSK) according to the North American system for *Pgt* race nomenclature (Jin et al., 2007; Jin et al., 2008). The unique virulence combination of *Pgt*-TTKSK allows this race to overcome resistance in the majority of wheat cultivars in Asia (Singh et al., 2008), the United States (Jin and Singh, 2006), and Canada (Fetch, 2007). In 2004, wheat scientists including Norman Borlaug witnessed an epidemic of stem rust in Kenya caused by *Pgt*-TTKSK. This observation was significant as it established that *Pgt*-TTKSK was not only virulent, but also aggressive. A global collaborative effort was then launched in order to rapidly address the threat of *Pgt*-TTKSK.

Subsequent monitoring of *Pgt*-TTKSK in Kenya identified two variants with additional virulence to resistance genes *Sr24* and *Sr36* (Jin et al., 2008; Jin et al., 2009).

These resistance genes are relatively widespread in the southern United States (Jin and Singh, 2006) increasing the threat of the *Pgt*-TTKSK race-complex. *Pgt*-TTKSK was found in Yemen in 2006 and in Iran in 2009 (Nazari et al., 2009). Accurate *Pgt* race analysis is needed in order to confirm presence or absence of *Pgt*-TTKSK so that growers and scientists know how imminent of a threat *Pgt*-TTKSK is to various wheat growing regions.

One inconsistency in *Pgt*-TTKSK race analysis has been whether or not virulence is present for *Sr21*. Initial seedling assays were inconclusive (Jin et al., 2007), and race analysis laboratories in the United States, Canada, and South Africa observe inconsistent reactions of *Pgt*-TTKSK and related races to monogenic lines with *Sr21*. Since *Sr21* is the second resistance gene in the North American differential set and inconsistent reactions are observed, *Pgt*-TTKSK has sometimes been classified as race PTKSK depending on a high or low infection type, respectively.

It has previously been reported that the degree of resistance conferred by *Sr21* varies with ploidy level (McIntosh et al., 1984). *Sr21* was not found to be temperature-sensitive to avirulent North American races (Roelfs and McVey, 1979). Our objective was to evaluate the sensitivity of the disease reaction between *Pgt*-TTKSK and variants to monogenic lines with *Sr21*.

Materials and methods

Eight wheat lines were used in this study (Table 2.1). CSA, LMPG-6, W2691, and PI 272557 are lines with no known stem rust resistance genes and are considered universally susceptible. CI 2433 (PI 10474) is a *T. monococcum* subsp. *monococcum* cultivar and is the diploid stock of *Sr21*, referred to as 'Einkorn' in Stakman et al. (1962). PI 272557 was characterized as a *T. monococcum* subsp. *monococcum* accession susceptible to five races of *Pgt* screened (Chapter 4).

Four to six plants of each line were inoculated with 15 isolates of *Pgt* corresponding to 14 races (Table 2.2). Four isolates of the *Pgt*-TTKSK race-complex were evaluated along with one North American isolate characterized as low on *Sr21* (race MCCFC) and ten North American isolates characterized as high on *Sr21*. Procedures in inoculation were followed as reported previously (Jin et al., 2007). After inoculation, plants were kept in one of five growth chamber environments: 16°C with a 15 hour photoperiod, 20°C with a 15 hour photoperiod, 24°C with a 15 hour photoperiod, 20°C with a 10 hour photoperiod, and 20°C with a 20 hour photoperiod. The disease infection types were scored 14 days after inoculation according to Stakman et al. (1962). Infection types were classified as low ranging between '0' and '2+' indicating host resistance and pathogen avirulence. Infection types '3-' to '4' were classified as high.

Field stem rust evaluations in Njoro, Kenya in 2008 and 2009 were conducted as previously reported (Jin et al., 2007). Infection response was categorized as R (resistant), MR (moderately resistant), MS (moderately susceptible), or S (susceptible) according to

Roelfs et al. (1992). Severity was assessed according to the modified Cobb scale (Peterson et al., 1948). Field phenotypic evaluations were performed multiple times during the growing season. The infection responses and severities recorded at the soft-dough growth stage are reported in this study.

Results

Seedling infection types

The infection types of the eight wheat lines against the 15 isolates in the five environments are displayed in Table 2.3. Overall, the *Pgt* isolates previously characterized as high on *Sr21*, all conferred high reactions to the *Sr21* monogenic lines in the different treatments. There were four exceptions to this. First, the disease response on CI 2433 was often intermediate regardless of the isolate or treatment. Second, *Pgt* race QCCLL was avirulent on LMPG-6 and DK13 in all treatments. Third, race QCCSM was avirulent on LMPG-6 and DK13 in the 16°C treatment. Since races QCCLL and QCCSM were avirulent to both DK13 and its recurrent parent, the resistance observed was independent of *Sr21*. Fourth, race QCCLL was avirulent both on W2691 and W3586 in the 24°C treatment. Again, this resistance appears to be independent of *Sr21*. Race MCCFC, previously characterized as avirulent on *Sr21*, was avirulent on the *Sr21* monogenic lines except in the 16°C treatment where obvious avirulence was only present on CI 2433. The infection types were intermediate on DK13 and W3586 and high on *T. monococcum* deriv.

Overall, the disease reaction between *Pgt*-TTKSK and related races to the *Sr21* monogenic lines and susceptible controls resembled the reaction of *Sr21*-avirulent race MCCFC. In the 16°C treatment, race TTKSK was high on the *Sr21* lines except for CI 2433 where an intermediate reaction was observed. Intermediate and high infection types were also observed on *T. monococcum* deriv. in the 20°C, 20 hour photoperiod treatment.

In the four other treatments, race TTKSK was avirulent on the *Sr21* monogenic lines with occasional intermediate reactions observed on *T. monococcum* deriv. The race TTKSK avirulent reaction on *Sr21* tended to result in slightly higher infection types than the race MCCFC avirulent reaction on *Sr21* across treatments.

Field response in Njoro, Kenya

Stem rust severities on control lines during 2009 were not as high as in previous years due to an extreme drought. Though the nursery was periodically irrigated, this moisture was not enough to facilitate overnight dew formation and plant growth similar to previous years.

Stem rust severities and infection responses on *Sr21* monogenic lines were equal to or slightly lower than the severities and infection responses on the susceptible controls (Table 2.4). The level of field resistance provided by *Sr21* was non-existent or slight. CI 2433 displayed a relatively low severity and infection response when included in the nursery in 2009. As we do not have field stem rust data for a diploid line with a genetic background similar to CI 2433 but without *Sr21*, the degree to which the resistance exhibited by CI 2433 was conferred by *Sr21* is not known.

Discussion

Our data indicate that the disease reaction between *Pgt*-TTKSK-related isolates and *Sr21* monogenic lines is temperature sensitive. The difference in infection types from 16°C to 20°C is dramatic, representing a range between clearly high infection types to clearly low infection types, respectively (Figure 2.1). Also, the reaction was influenced by genetic background exemplified by the slightly higher reactions often observed on *T. monococcum* deriv. compared to the other monogenic lines against *Pgt*-TTKSK-related isolates. The slightly higher infection types observed on *T. monococcum* deriv. in the 20°C, 20 hour photoperiod treatment indicated that light may also play a role in this environmentally-sensitive reaction.

The infection types of the *Pgt*-TTKSK-related isolates were similar to the race MCCFC infection types across treatments, demonstrating that the *Pgt*-TTKSK-related isolates are most accurately described as avirulent on *Sr21*. However, avirulence on *Sr21* was found to be temperature sensitive for both race MCCFC and the *Pgt*-TTKSK-related isolates. Avirulence on *Sr21* was not previously described as being temperature sensitive by Roelfs and McVey (1979). It is likely that previous experiments did not examine disease reactions in the same range of temperatures (the range of temperatures tested previously is not described (Roelfs and McVey, 1979)). Also, since the *Pgt*-TTKSK-related isolates tended to confer slightly higher infection types than race MCCFC and we observed race MCCFC avirulence to be less temperature sensitive, the avirulent isolates of *Pgt* used by Roelfs and McVey (1979) could be less temperature-sensitive than

TTKSK. Slight differences in avirulence among races have been reported previously (Watson and Luig, 1968). Similarly to our study, the progressive increases in virulence were observed on a temperature sensitive gene, *Sr6*. Interestingly, *Sr6* was demonstrated to be light-sensitive as well as temperature-sensitive (Forsyth, 1956).

Races QCCLL and QCCSM were avirulent on LMPG-background lines. The resistance observed to QCCSM was temperature-sensitive, effective only at the 16°C treatment. The treatment of the eight lines inoculated with QCCSM at 16°C was repeated, and the same result was found. Similarly, race QCCLL was avirulent on W2691 and W3586 only at the 24°C treatment. Both QCCLL and QCCSM were collected from Washington, USA. Previous studies indicated that various isolates of *Pgt* from Washington, USA were avirulent on lines considered to be universally susceptible (Rouse et al., 2009).

CI 2433 was included in the original stem rust differential set described by Stakman et al. (1962). We observed intermediate reactions on CI 2433 against several *Sr21*-virulent races. It is possible that the generally lower infection types on CI 2433 could be due to additional resistance gene(s) in this diploid stock. Infection types on CI 2433 against *Sr21*-avirulent isolates were generally lower than on the other monogenic lines and CI 2433 was more resistant than the other *Sr21* monogenic lines in the field. This result is likely due to the higher effectiveness of *Sr21* at lower ploidy levels (The, 1973b). However, if additional resistance genes are present in CI 2433, these genes could confer the lower infection types and field reaction observed. We have crossed CI 2433 and PI 272557 in order to examine the genetics of resistance in CI 2433 to *Sr21*-virulent

races of *Pgt* in addition to various *Pgt*-TTKSK-related isolates. Plants from $F_{2:3}$ families are currently being screened for this purpose.

The field stem rust evaluations indicate that *Sr21* confers modest to no resistance to *Pgt*-TTKSK-related races present in Njoro, Kenya. Therefore, gene *Sr21* should not be used as the only source of resistance to Ug99 in a wheat line. However, the results of this study are significant in elucidating that *Pgt*-TTKSK-related isolates are avirulent on *Sr21* in a temperature-sensitive manner. Our data explain why *Pgt*-TTKSK-related isolates are inconsistently classified as virulent on *Sr21* by race-analysis laboratories worldwide. Currently, *T. monococcum* deriv. is used as the *Sr21* monogenic line for *Pgt* race analysis conducted at the United States Department of Agriculture Cereal Disease Laboratory (Jin et al., 2008). Since, *T. monococcum* deriv. resistance to *Pgt*-TTKSK is the most sensitive to temperature relative to the other *Sr21* lines, caution should be taken when characterizing *Pgt* races when using this differential line.

Our data indicate that the isolates used in this study corresponding to races TTKSK, TTKST, and TTTSK could be more accurately described as races PTKSK, PTKST, and PTTSK, respectively, based on their demonstrated avirulence to *Sr21*. However, environmental conditions in greenhouses used for race analysis in the winter at the Cereal Disease Laboratory in St. Paul, Minnesota often result in high infection types observed for *Pgt*-TTKSK-related isolates against *Sr21* monogenic lines in the background of Chinese Spring. A recent study discriminated among *Pgt*-TTKSK-related isolates on the basis of reaction to *Sr21* (Pretorius et al., 2010). However, isolates classified as both high and low on *Sr21* in that study exhibited low infection types on CI

2433, with the isolate classified as race TTKSK exhibiting a ‘2’ infection type on CI 2433. Isolates classified as race PTKSK exhibited a ‘;1’ infection type on CI 2433. There are two ways to interpret these results. First, environmental variability may be accounting for the differences in infection types observed on *Sr21* in race TTKSK and race PTKSK isolates. Second, there may be isolates from South Africa that are lower on CI 2433 than the isolates available to us. Further studies repeating the results reported in Pretorius et al. (2010) and examining the genetics of resistance of CI 2433 to isolates classified as race TTKSK and race PTKSK are needed.

Table 2.1. *Sr21* monogenic lines and susceptible controls

Line	Genome	Pedigree	Resistance Gene	Reference
Chinese Spring	AABBDD	-	none	-
Triticum monococcum L. derivative	AABBDD	W1569/C68-123//Chinese Spring	*Sr21*	The, 1973; Roelfs and McVey, 1979
LMPG-6	AABBDD	Prelude/8*Marquis	none	Knott, 1990
DK13	AABBDD	T. mono deriv./8*LMPG	*Sr21*	Knott, 1990
W2691	AABBDD	Little Club//Gabo/Charter	none	Watson and Luig, 1963
W3586	AABBDD	Glossy Hugenot/C68.123//unknown hexaploid	*Sr21*	The, 1973
PI 272557	A^mA^m	-	none	Chapter 4, 5
CI 2433	A^mA^m	-	*Sr21*	Chapter 4, 5

Table 2.2. Avirulence/virulence formulae for isolates of *Puccinia graminis* f. sp. *tritici*

Isolate	Race	Origin	Avirulence	Virulence
04KEN156/04	TTKSK[a]	Kenya	24 36 Tmp	5 6 7b 8a 9a 9b 9d 9e 9g 10 11 17 30 31 38 McN
09KEN09-2	TTKSK	Kenya	24 36 Tmp	5 6 7b 8a 9a 9b 9d 9e 9g 10 11 17 30 31 38 McN
06KEN19V3	TTKST	Kenya	36 Tmp	5 6 7b 8a 9a 9b 9d 9e 9g 10 11 17 24 30 31 38 McN
07KEN24-4	TTTSK	Kenya	24 Tmp	5 6 7b 8a 9a 9b 9d 9e 9g 10 11 17 30 31 36 38 McN
06YEM34-1	TRTTF	Yemen	8a 24 31	5 6 7b 9a 9b 9d 9e 9g 10 11 17 21 30 36 38 McN Tmp
01MN84A-1-2	TTTTF	Minnesota	24 31	5 6 7b 8a 9a 9b 9d 9e 9g 10 11 17 21 30 36 38 McN Tmp
74MN1409	TPMKC	Minnesota	6 9a 9b 24 30 31 38	5 7b 8a 9d 9e 9g 10 11 17 21 36 Tmp McN
06ND717C	QFCSC	North Dakota	6 7b 9b 9e 11 24 30 31 36 38 Tmp	5 8a 9a 9d 9g 10 17 21 McN
99KS76A-1	RKQQC	Kansas	9e 10 11 17 24 30 31 38 Tmp	5 6 7b 8a 9a 9b 9d 9g 21 36 McN
75ND717C	QTHJC	North Dakota	7b 9a 9e 24 30 31 36 38 Tmp	5 6 8a 9b 9d 9g 10 11 17 21 McN
77ND82A-1	RCRSC	North Dakota	6 8a 9e 11 24 30 31 38 Tmp	5 7b 9a 9b 9d 9g 10 17 21 36 McN
07WA140-17-1	QCCLL	Washington	6 7b 8a 9b 9d 9e 10 11 30 31 36 38 Tmp McN	5 9a 9g 17 21 24
75WA165-2A	QCCSM	Washington	6 7b 8a 9b 9e 11 30 31 36 38 Tmp	5 9a 9d 9g 10 17 21 24 McN
09ID73-2	SCCSC	Idaho	6 7b 8a 9b 11 24 30 31 36 38 Tmp	5 9a 9d 9e 9g 10 17 21 McN
59KS19	MCCFC	Kansas	6 8a 9a 9b 9d 9e 11 21 24 30 31 36 38	5 7b 9g 10 17 Tmp McN

[a] *Sr21* is not included in the formula for *Pgt*-TTKSK-related races.

Table 2.3. Seedling infection types of lines with and without *Sr21* to diverse isolates of *Puccinia graminis* f. sp. *tritici* at various temperatures and photoperiods

Line	Temp.[a] celcius	Photo.[b] hours	TTKSK[c]	TTKSK[d]	TTKST	TTTSK	MCCFC
Chinese Spring	16	15	3+	3+	3+	3+	3
Chinese Spring	20	15	3+	3+	3+	3+	3+
Chinese Spring	24	15	4	4	3+	4	4
Chinese Spring	20	10	4	3+	3+	3+	33+
Chinese Spring	20	20	4	4	3+	-	3+
T. monococcum deriv.	16	15	3+	3+	3+	3+	3
T. monococcum deriv.	20	15	2+3	2+3-	2+3-	2	2-
T. monococcum deriv.	24	15	22+	2+3-	2	2-	12-
T. monococcum deriv.	20	10	2+3-	2+	2	2-	2-
T. monococcum deriv.	20	20	32+	3+	32+	-	2
LMPG-6	16	15	3+	3+	3+	-	3+
LMPG-6	20	15	4	4	3+	3+	33+
LMPG-6	24	15	3+	4	3+	4	3+
LMPG-6	20	10	3+	3+	3+	3+	3
LMPG-6	20	20	3+	4	3+	3+	3+
DK13	16	15	3+	3	3+	3+	23-
DK13	20	15	2	2	2	2-	2-
DK13	24	15	2	2	2	2	2-
DK13	20	10	2	2	2	2	2-
DK13	20	20	2	2+3-	22+	2	2-
W2691	16	15	3	3+	3+	-	3+
W2691	20	15	4	3+	4	3+	4
W2691	24	15	4	4	4	4	4
W2691	20	10	4	3+	4	3+	33+
W2691	20	20	4	3+	3+	3+	3+
W3586	16	15	3+	3+	3+	-	23-
W3586	20	15	2	2	2-	-	2-
W3586	24	15	2-	2	2-	2	1
W3586	20	10	2	2	2	2-	2-
W3586	20	20	22+	2+	-	2-	2
PI 272557	16	15	3+	3+	3	3+	3
PI 272557	20	15	3	3	3+	3+	2+3
PI 272557	24	15	3+	4	3+	3+	3+
PI 272557	20	10	3+	3+	33+	3+	3
PI 272557	20	20	3+	3+	3+	-	3+
CI 2433	16	15	2+3	2+3	2+3	3	1
CI 2433	20	15	2-	2-	2-	;2-	12-
CI 2433	24	15	2-	2-	2-	2-	;1
CI 2433	20	10	2-	2-	2-	2-	2=;
CI 2433	20	20	2-2	22+	2	2-	12-

Table 2.3 continued.

Line	Temp.[a] celcius	Photo.[b] hours	TRTTF	TTTTF	TPMKC	QFCSC	RKQQC
Chinese Spring	16	15	4	4	4	3+	4
Chinese Spring	20	15	3+	4	3+	3+	3+
Chinese Spring	24	15	3+	3+	3+	3+	3+
Chinese Spring	20	10	3+	3+	3+	3+	3+
Chinese Spring	20	20	4	3+	4	3+	4
T. monococcum deriv.	16	15	4	4	4	3+	4
T. monococcum deriv.	20	15	3+	3+	3+	3+	3+
T. monococcum deriv.	24	15	3+	3+	3+	3+	3+
T. monococcum deriv.	20	10	3+	3+	3	3	3
T. monococcum deriv.	20	20	4	3+	4	3+	4
LMPG-6	16	15	4	3+	4	3	4
LMPG-6	20	15	3+	3+	3+	33+	3+
LMPG-6	24	15	3+	3+	4	3	3+
LMPG-6	20	10	3+	3	3-3	3	3+
LMPG-6	20	20	4	4	4	3+	4
DK13	16	15	4	3+	4	3	4
DK13	20	15	3+	3+	3+	33+	3+
DK13	24	15	3+	3+	3+	3+	3+
DK13	20	10	3+	3	3-3	3	3+
DK13	20	20	4	3+	4	3+	4
W2691	16	15	4	3+	4	4	4
W2691	20	15	3+	4	4	4	3+
W2691	24	15	4	3+	4	4	4
W2691	20	10	4	3+	3+	4	3+
W2691	20	20	4	3+	4	4	4
W3586	16	15	4	3+	4	3+	4
W3586	20	15	3+	4	3+	3+	3+
W3586	24	15	3+	3+	3+	4	3
W3586	20	10	3+	3+	3+	3+	3+
W3586	20	20	3+	3+	4	3+	4
PI 272557	16	15	4	3+	3+	3+	-
PI 272557	20	15	3+	3+	3+	3+	33+
PI 272557	24	15	3+	3	3+	3+	3+
PI 272557	20	10	3+	-	3-3	3	3
PI 272557	20	20	-	3	3+	3+	3+
CI 2433	16	15	3+	2+3	2+3	3	2+3
CI 2433	20	15	2+3	3+	2+3+	33+	2+3
CI 2433	24	15	33+	33+	3	3	2+3
CI 2433	20	10	3	3	3-	2+3	2+3
CI 2433	20	20	2+3+	3+	3	2+3	2+3+

Table 2.3 continued.

Line	Temp.[a] celcius	Photo.[b] hours	QTHJC	RCRSC	QCCLL	QCCSM	SCCSC
Chinese Spring	16	15	3+	3+	3+	4	3+
Chinese Spring	20	15	4	3+	4	3+	3+
Chinese Spring	24	15	4	3+	3+	3+	3+
Chinese Spring	20	10	4	3+	4	3+	3+
Chinese Spring	20	20	3+	3+	3+	3+	4
T. monococcum deriv.	16	15	4	3+	3+	4	3+
T. monococcum deriv.	20	15	4	3+	3+	3+	3+
T. monococcum deriv.	24	15	3+	3+	3+	3+	3+
T. monococcum deriv.	20	10	4	3+	3+	3+	3+
T. monococcum deriv.	20	20	3+	3+	3+	3+	4
LMPG-6	16	15	3+	3+	2	;13-	3+
LMPG-6	20	15	3+	3+	2	3+	3+
LMPG-6	24	15	3+	3+	2	3+	3+
LMPG-6	20	10	3+	3+	2+	3+	3+
LMPG-6	20	20	3+	3+	2+3	3+	3+
DK13	16	15	3+	3+	2	;1+	3+
DK13	20	15	3+	3+	2	3+	3+
DK13	24	15	3+	3+	2	3+	3+
DK13	20	10	3+	3+	22+	3+	3+
DK13	20	20	3+	3+	2+	3+	3+
W2691	16	15	4	3+	3+	4	4
W2691	20	15	4	4	3	3+	3+
W2691	24	15	4	3+	2	4	4
W2691	20	10	4	3+	3	4	3+
W2691	20	20	4	3+	3+	4	4
W3586	16	15	X	3	3+	3+	3+
W3586	20	15	3+	-	3+	3+	3+
W3586	24	15	3+	2+3	2+3	3+	3+
W3586	20	10	3+	-	3	3+	33+
W3586	20	20	3+	3+	3+	3+	3+
PI 272557	16	15	3	3+	-	3+	-
PI 272557	20	15	-	3+	-	-	-
PI 272557	24	15	3+	-	3	3+	-
PI 272557	20	10	-	3+	-	-	33+
PI 272557	20	20	3+	-	3+	3+	-
CI 2433	16	15	33+	2+3	2+3	2+3-	2+3
CI 2433	20	15	2+3	-	2+3	23	2+3
CI 2433	24	15	2+3	2+3	2+3	2+3	3
CI 2433	20	10	2+3	3	2+3	2+3	3
CI 2433	20	20	2+3+	2+3	2+3	2+3+	3

Table 2.3 continued.

[a] Temperature

[b] Photoperiod

[c] 04KEN156/04

[d] 09KEN09-2

Table 2.4. Field reaction of monogenic lines with *Sr21* and susceptible controls to *Puccinia graminis* f. sp. *tritici* in Njoro, Kenya

	Year			
Line	**2005**	**2006**	**2008**	**2009**
Chinese Spring	80 S	80 S	80 S	60 S
T. mono. deriv.	70 S	80 S	70 S	60 MS-S
LMPG-6	60 MS-S	60 S	70 S	60 S
DK13	-	30 MS-S	70 MS-S	50 MS-S
W3586	-	-	60 MS	40 MS-S
CI 2433	-	-	-	20 MR-MS

A

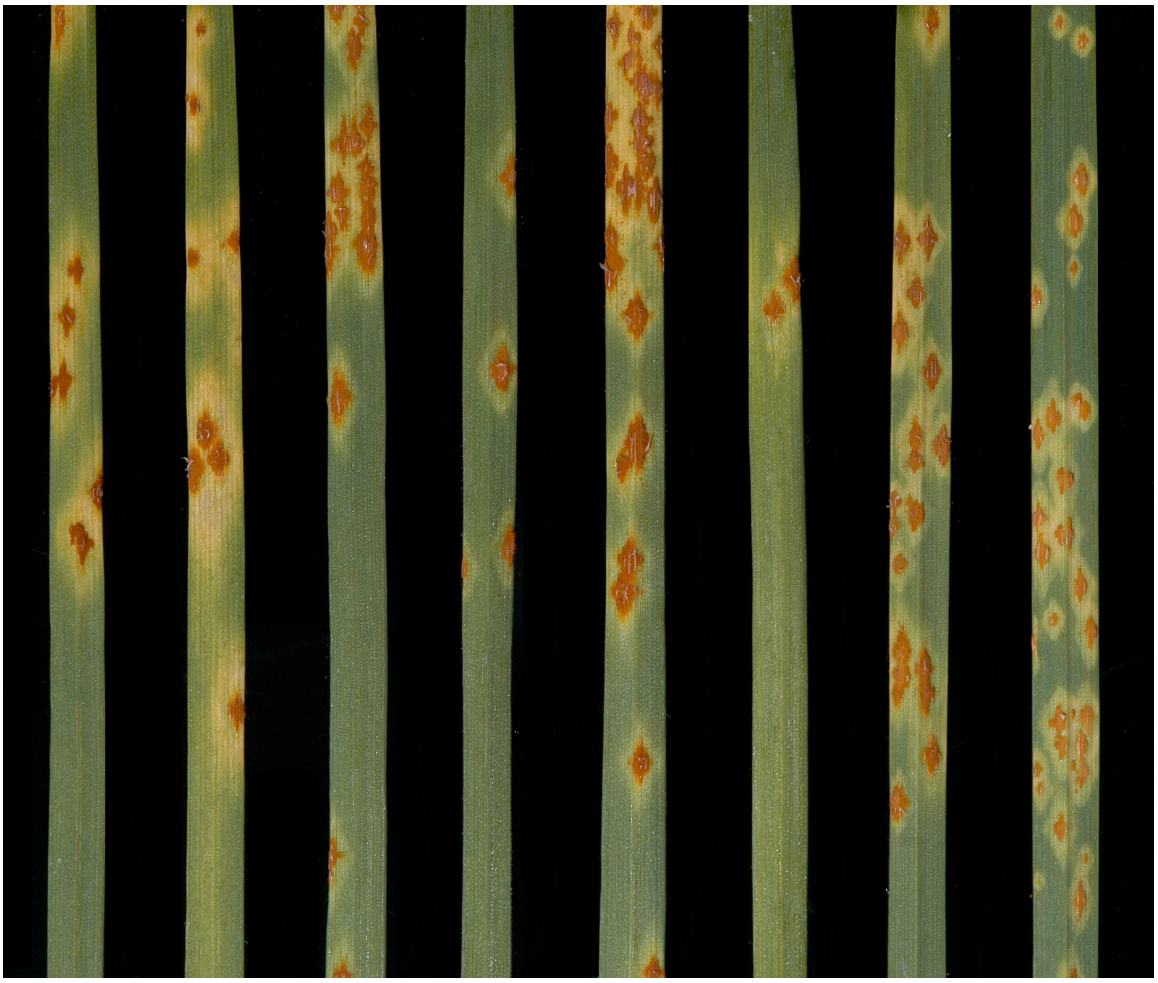

Figure 2.1. Reaction of Chinese Spring, *T. monococcum* deriv., LMPG-6, DK13, W2691, W3586, PI 272557, and CI 2433 (from left to right respectively) to *Pgt* race TTKSK at 16°C with a 15 hour photoperiod (A) and 20°C with a 15 hour photoperiod (B)

B

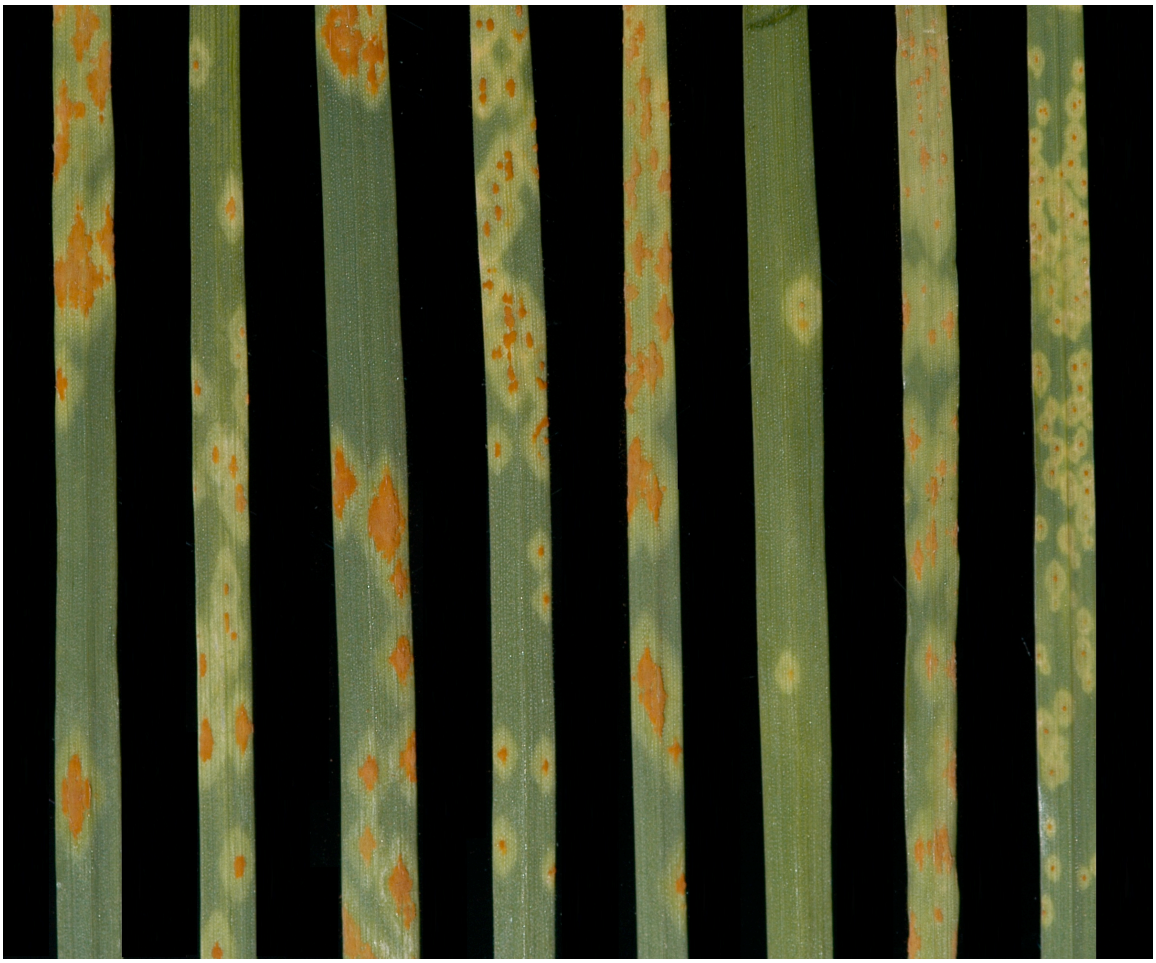

Figure 2.1 continued.

Chapter III

Stem rust resistance in *Aegilops tauschii* germplasm

Summary

Aegilops tauschii Cosson, the D genome donor of hexaploid wheat, *Triticum aestivum* L., has been used extensively for the transfer of agronomically important traits to wheat, including stem rust resistance genes *Sr33*, *Sr45*, and *Sr46*. In order to identify potentially new stem rust resistance genes in *Ae. tauschii* germplasm, 456 non-duplicated accessions deposited in the USDA National Small Grains Collection (Aberdeen, ID) and the Wheat Genetic and Genomic Resources Center collection (Kansas State University, Manhattan, KS), were evaluated with races TTKSK (Ug99), TRTTF, TTTTF, TPMKC, QTHJC, and RKQQC of *Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks. & E. Henn. (*Pgt*). Ninety-eight accessions (22%) were identified as resistant to *Pgt*-TTKSK. A broad range of low infection types (';' to '2+') were found in response to *Pgt*-TTKSK. Resistance was significantly associated among most of the races in pair-wise comparisons. However, resistance was largely race-specific. Only 12 of the accessions resistant to *Pgt*-TTKSK were also resistant to the other five races. Results from this germplasm screening will facilitate further studies on the genetic characterization of accessions with potentially new sources of resistance to *Pgt*-TTKSK.

Introduction

Aegilops tauschii Cosson is the donor of the D genome of hexaploid wheat, *Triticum aestivum* L. (Kihara, 1944). Wheat stem rust, caused by *Puccinia graminis* Pers.:Pers f. sp. *tritici* Eriks. & E. Henn. (*Pgt*), has historically been a major wheat yield-limiting factor. The close relationship between *A. tauschii* and *T. aestivum* has facilitated the rapid introgression of several agronomically important disease traits from *A. tauschii* to *T. aestivum* including resistance to wheat stem rust (Kerber and Dyck, 1979; Marais et al., 1998).

Recent epidemics of stem rust in Eastern Africa have raised concern about the resistance of currently grown wheat cultivars to new races of *Pgt*. In 1999, a race was reported from Uganda that possessed virulence to the majority of stem rust resistance genes used in agriculture (Pretorius et al. 2000). This race was designated as TTKSK (or Ug99, *Pgt*-TTKSK) based upon the North American stem rust nomenclature (Jin et al., 2008). *Pgt*-TTKSK has spread throughout Eastern Africa, Yemen, and Iran (Singh et al., 2006; Nazari et al., 2009). Variants of *Pgt*-TTKSK have been identified with additional virulence to stem rust resistance genes *Sr24* and *Sr36* (Jin et al., 2008; Jin et al., 2009). These variants (races TTKST and TTTSK, respectively) pose an even greater threat to worldwide wheat production. Screening of currently grown cultivars and breeding germplasm indicated that the majority of the germplasm from Asia, the United States, and Canada are susceptible to *Pgt*-TTKSK (Jin and Singh, 2006; Fetch 2007; Singh et al., 2008). Unfortunately, much of the resistance to *Pgt*-TTKSK available in the United

States is conferred by *Sr24* and *Sr36* (these genes are not effective to races TTKST and TTTSK, respectively). Of the available sources of resistance to TTKSK and variants described to-date, most resistance genes have been introgressed from wild relatives of wheat (Jin et al., 2007) and have not been utilized extensively in agriculture because of linkage between these genes and deleterious factors (Singh et al., 2008).

Three stem rust resistance genes have been transferred from *Ae. tauschii* to wheat previously: *Sr33*, *Sr45*, and *Sr46* (Kerber and Dyck, 1979; Marais et al., 1998; Lagudah, *unpublished*). These genes provide resistance to *Pgt*-TTKSK (Jin et al., 2007; Rouse and Jin *unpublished*). Additional resistance genes may be present in *Ae. tauschii* germplasm. The identification of new genes will provide breeders with additional genes for pyramiding in order to increase the durability of resistance. Our objective was to screen the available accessions of *Ae. tauschii* for resistance to *Pgt*-TTKSK in order to facilitate the characterization and introgression of new resistance.

Materials and methods

Aegilops tauschii accessions were obtained from the USDA-ARS Germplasm Resources Information Network, National Small Grains Collection (GRIN, NSGC, Aberdeen, ID, 118 accessions) and from the Wheat Genetic and Genomic Resources Center (WGGRC, Manhattan, KS, 412 accessions). The accession names and sources were cross-checked in order to eliminate accessions that were redundant among or within the two collections. We identified 456 non-redundant accessions. The geographic origins of these accessions are displayed in Table 3.1.

Six to ten seedlings of the 456 accessions were inoculated with six races of *Pgt*: TRTTF, TTKSK, TTTTF, QTHJC, RKQQC, and TPMKC (Table 3.2). Screening with TRTTF, TTKSK, and TTTTF was completed at the USDA-ARS Cereal Disease Laboratory (Saint Paul, MN). Screening with QTHJC, RKQQC, and TPMKC was completed at the Department of Plant Pathology, Kansas State University (Eric Olson and Mike Pumphrey, Manhattan, KS). Accessions that have been used previously to introgress stem rust resistance genes *Sr33* and *Sr45*, RL5288 and RL5289, respectively, were obtained from Colin Heibert (Agriculture and Agri-Food Canada, Winnipeg, Manitoba). The diploid *Ae. tauschii* source of *Sr46* (AUS 18913) and genetic stocks of *Sr33* and *Sr45* in hexaploid backgrounds were obtained from CSIRO (CSID 5404 and CSID 5406, respectively). These stocks and susceptible Chinese Spring were inoculated with the six *Pgt* races. Urediniospores of stem rust isolates in gelatin capsules stored at

-80°C were heat-shocked at 45°C for 15 min, and placed in a rehydration chamber for 2 to 4 h maintained at 80% relative humidity by a KOH solution (Rowell, 1984). Procedures of inoculation, incubation and disease assessment were performed as described previously (Jin et al. 2007). Infection types (ITs) were classified as in Stakman et al. (1962) with the following modifications for evaluating *Ae. tauschii*. Infection types with substantial necrosis or chlorosis were designated as "N" or "C", respectively. When infection frequency was notably low, the IT was designated as "LIF" indicating low infection frequency. ITs '0' to '2++' were considered low ITs indicating host resistance whereas ITs '3=' to '4' were considered high ITs indicating host susceptibility. When low and high ITs were present on the same leaf, the reaction was considered mesothetic and the plant was classified as resistant (McIntosh et al., 1995). Accessions that segregated for resistance were considered heterogeneous.

Frequencies of resistant, susceptible, and heterogeneous accessions were calculated for each of the six races. For each accession, the reaction to the combined races was considered as susceptible if the IT to any of the six races was high, resistant if the ITs to all six races was low, and heterogeneous if the reaction to one of the races was heterogeneous and the reaction to the five other races was low or heterogeneous. In order to test for associations of resistance, we calculated chi-square values based on the assumption of independence of resistance to each race for every pair-wise comparison of races. Heterogeneous accessions were not included in association analyses because their small sample sizes violated conditions necessary for chi-square tests.

Results

The seedling infection types of the *Ae. tauschii* accessions are recorded in Appendix I. The frequencies of accessions resistant, susceptible, and heterogeneous to the six races are displayed in Table 3.3. Ninety-eight accessions (22.2%) were resistant to *Pgt*-TTKSK, but only 12 of these accessions (2.7%) were resistant to the five other races as well. Race TRTTF was the most virulent race on this germplasm (88.2% of the accessions were susceptible) whereas race QTHJC was the most avirulent (68.0% of the accessions were susceptible). Relatively few of the accessions were heterogeneous to any of the races (0.5% to 2.1%).

The diploid genetic stocks of *Sr33*, *Sr45*, and *Sr46* (RL5288, RL5289, and AUS 18913, respectively) displayed unique infection type patterns to the races screened (Table 3.4). The diploid source of *Sr46* was also included in the germplasm screening (TA 1703 is synonymous with AUS 18913).

Significant associations were found for all race pair-wise comparisons except for races TTTTF and RKQQC (Table 3.5). However, diverse IT patterns were observed indicating the presence of multiple race-specific resistance genes.

Discussion

Previous studies have examined collections of *Ae. tauschii* or synthetic hexaploid wheats created with *Ae. tauschii* accessions for resistance to stem rust (Assefa and Fehrmann, 2004; Friesen et al., 2008; Ogbonnaya et al., 2008). We evaluated a relatively large collection of *Ae. tauschii* accessions in an attempt to identify resistance to *Pgt*-TTKSK.

In a worldwide survey of *Pgt* virulence, isolates with virulence to *Sr33* were not found (Huerta-Espino, 1992). Seedling and adult plant resistance of hexaploid monogenic lines carrying *Sr33* to race TTKSK is only moderate (Jin et al., 2007). Gene *Sr33* will need to be combined with additional sources of resistance to *Pgt*-TTKSK to provide adequate field resistance. The dilution of *Ae. tauschii* resistance when expressed in hexaploids (Kerber and Dyck, 1979) may be one reason why *Sr33* resistance to *Pgt*-TTKSK is moderate. The level of adult plant resistance to *Pgt*-TTKSK conferred by *Sr45* and *Sr46* is unknown. *Sr45* is ineffective to the predominant races in North America (Table 3.4; Kerber and Dyck, 1979; Marais et al., 1998). Our data indicate that *Sr46* resistance is race-specific (Table 3.4). If *Sr45* and *Sr46* are used to provide resistance to *Pgt*-TTKSK, additional resistance genes will be necessary to provide resistance to other *Pgt* races.

We interpret the significant associations of resistance to various races observed as evidence for genes conferring resistance to multiple races. However, only 12 accessions were resistant to the six races. Diverse IT patterns were observed among the *A. tauschii*

accessions. The diversity of IT patterns prevented us from being able to confidently postulate the presence of known genes in the germplasm screened and indicate possible diversity for genes, modifier genes, or genetic background effects. The IT patterns of a subset of accessions with unknown genes are displayed in Table 4. Many IT patterns could not be accounted for by the previously described genes alone or in combination. This suggests that additional stem rust resistance genes are likely present in *Ae. tauschii* germplasm. As *Sr33* provides resistance to all six races, further studies are needed to test the allelic relationship between *Sr33* and resistance in the 12 accessions that were characterized as resistant to all races tested. Preliminary evidence based on ITs suggest that accessions with resistance to all races screened possess a gene (or genes) independent of *Sr33*. For example, accession TA 10171 exhibited resistance to the six races with ITs much lower than observed on *Ae. tauschii* accession RL5288 (*Sr33*; Table 3.4). Further studies testing the allelic relationship between previously described genes and potentially new resistance are needed to confirm the presence of new resistance to *Pgt*-TTKSK specifically. Crosses have been made to confirm the presence of new resistance to *Pgt*-TTKSK, map potentially new sources of resistance, and introgress such resistance.

Table 3.1. Geographic origin of *Aegilops tauschii* accessions

Country	Accessions
Afghanistan	83
Armenia	21
Azerbaijan	43
China	18
Former USSR	4
Georgia	14
Iran	67
Kazakhstan	8
Kyrgyzstan	4
Pakistan	10
Russia	3
Syria	5
Tajikistan	41
Turkey	31
Turkmenistan	45
Uzbekistan	30
Unknown	29

Table 3.2. Races of *Puccinia graminis* f. sp. *tritici* used to screen *Aegilops tauschii* germplasm

Isolate	Race	Origin	Avirulence	Virulence
04KEN156/04	TTKSK [a]	Kenya	*24 36 Tmp*	*5 6 7b 8a 9a 9b 9d 9e 9g 10 11 17 30 31 38 McN*
06YEM34-1	TRTTF	Yemen	*8a 24 31*	*5 6 7b 9a 9b 9d 9e 9g 10 11 17 21 30 36 38 McN Tmp*
01MN84A-1-2	TTTTF	US	*24 31*	*5 6 7b 8a 9a 9b 9d 9e 9g 10 11 17 21 30 36 38 McN Tmp*
75ND717C	QTHJC	US	*7b 9a 9e 24 30 31 36 38 Tmp*	*5 6 8a 9b 9d 9g 10 11 17 21 McN*
99KS76A-1	RKQQC	US	*9e 10 11 17 24 30 31 38 Tmp*	*5 6 7b 8a 9a 9b 9d 9g 21 36 McN*
74MN1409	TPMKC	US	*6 9a 9b 24 30 31 38*	*5 7b 8a 9d 9e 9g 10 11 17 21 36 Tmp McN*

[a] *Sr21* is not included in the formula for race TTKSK.

Table 3.3. Number (and frequency) of *Aegilops tauschii* accessions resistant, susceptible, and heterogeneous to six *Puccinia gramnis* f. sp. *tritici* races and the combined reaction to the six races

Race	Total	Resistant (%)	Susceptible (%)	Heterogeneous (%)
TRTTF	439	48 (10.9%)	387 (88.2%)	4 (0.91%)
TTKSK	442	98 (22.2%)	338 (76.5%)	6 (1.36%)
TTTTF	436	61 (14.0%)	366 (83.9%)	9 (2.06%)
QTHJC	413	130 (31.5%)	281 (68.0%)	2 (0.48%)
RKQQC	422	121 (28.7%)	299 (70.9%)	2 (0.47%)
TPMKC	423	95 (22.5%)	326 (77.1%)	2 (0.47%)
Combined	448	12 (2.68%)	432 (96.4%)	4 (0.89%)

Table 3.4. Infection types of *Aegilops tauschii* accessions with known stem rust resistance genes and selected lines with unknown genes

Accession	Background	Gene	TRTTF	TTKSK	TTTTF	QTHJC	RKQQC	TPMKC
Chinese Spring	*T. aestivum*	-	4	4	4	3	4	4
RL5288	*A. tauschii*	*Sr33*	-	-	2/2,2+	2	;,2-	2
CSID 5405	*T. aestivum*	*Sr33*	-	2++	-	22-	2+	22+
RL5289	*A. tauschii*	*Sr45*	-	-	4	4	4	4
CSID 5406	*T. aestivum*	*Sr45*	4	0;	4	3	4	3+
TA 1703	*A. tauschii*	*Sr46*	2	;,2-	4	2-	2++	1,;
AUS 18913	*A. tauschii*	*Sr46*	2	;,1,2-	3+	3	3+	2-
TA 10087	*A. tauschii*	-	1	;,2-	;,1C	;,1	3-	1
TA 10124	*A. tauschii*	-	1,2	1,1+	1,2-,3-	;,1	3,2++	2,2-
TA 10147	*A. tauschii*	-	4	;,1N	;,1N	1-,2	;0	;0
TA 10171	*A. tauschii*	-	;	;	0;	0	0,;	;
TA 10206	*A. tauschii*	-	3+	;,1	1,3-Z	;,1	;,1=	;,1=
CIae 15	*A. tauschii*	-	2+,3	1,2-;	4	3+,4	2-	3

Table 3.5. Pair-wise comparisons of the association between reactions to six *Puccinia gramnis* f. sp. *tritici* races

Association between			Association	
Race	**Race**	χ^2	**Type**[a]	***P* value**
TRTTF	TTKSK	150.65	+	1.91 E-32
TRTTF	TTTTF	59.68	+	6.87 E-13
TRTTF	QTHJC	86.72	+	1.11 E-18
TRTTF	RKQQC	37.024	+	4.55 E-08
TRTTF	TPMKC	114.27	+	1.32 E-24
TTKSK	TTTTF	36.77	+	5.16 E-08
TTKSK	QTHJC	92.34	+	6.89 E-20
TTKSK	RKQQC	63.65	+	9.76 E-14
TTKSK	TPMKC	138.93	+	6.42 E-30
TTTTF	QTHJC	129.32	+	7.59 E-28
TTTTF	RKQQC	6.04	ns	0.11
TTTTF	TPMKC	37.44	+	3.72 E-08
QTHJC	RKQQC	51.98	+	3.02 E-11
QTHJC	TPMKC	130.32	+	4.61 E-28
RKQQC	TPMKC	101.31	+	8.13 E-22

[a] For significant associations, '+' indicates a positive association among resistant accessions and '-' indicates a negative association among resistant accessions. Symbol 'ns' indicates a non-significant association.

Chapter IV

Stem rust resistance in A-genome diploid relatives of wheat

Summary

Wheat stem rust, caused by *Puccinia graminis* f. sp. *tritici* (*Pgt*), has been effectively controlled through the use of genetic resistance. The recently identified race TTKSK (Ug99) possesses virulence to many resistance genes that have been used in wheat breeding worldwide. One strategy to aid breeders in developing resistant varieties is to utilize resistance genes transferred from wild relatives to wheat. Stem rust resistance genes have previously been introgressed from *Triticum monococcum* to wheat. In order to identify additional resistance genes, we screened 1061 accessions of *T. monococcum* and 214 accessions of *T.urartu* with *Pgt*-TTKSK and four additional races: TTTTF, TRTTF, QFCSC, and MCCFC. A large proportion of the accessions (78.7%, of *T. monococcum* and 93.0% of *T. urartu*) were resistant to *Pgt*-TTKSK with infection types ranging from '0' to '2+'. Among these resistant accessions, 55 *T. monococcum* accessions (6.4% of the total) were also resistant to the other four races. Associations of resistance to different races in *T. monococcum* indicated the presence of genes conferring resistance to multiple races. Comparing the infection type patterns observed to the expected patterns of known genes indicated that previously uncharacterized resistance genes to *Pgt*-TTKSK exist in both *T. monococcum* and *T. urartu*.

Introduction

Puccinia graminis f. sp. *tritici* (*Pgt*), the causal agent of wheat stem rust, has caused major yield losses throughout history. Over the past several decades, wheat stem rust has been effectively controlled worldwide through the deployment of resistant cultivars. Many of these resistant cultivars carry resistance gene *Sr31*. In Uganda in 1999, a race of *P. graminis* f. sp. *tritici* (Ug99) was characterized as virulent to *Sr31* and many other stem rust resistance genes (Pretorius et al., 2000). Ug99 is identified as *Pgt* race TTKSK based on the North American stem rust nomenclature (*Pgt*-TTKSK; Jin et al., 2008). *Pgt*-TTKSK has subsequently spread throughout Eastern Africa (Singh et al., 2006), Yemen, and Iran (Nazari et al., 2009). In 2006, a variant of *Pgt*-TTKSK was found in Kenya that possesses virulence to *Sr24* (race TTKST, Jin et al., 2008). In 2007, a variant with virulence to *Sr36*, designated as race TTTSK, was detected in Kenya (Jin et al., 2009).

Preliminary tests conducted in Kenya suggested that nearly all of the current wheat cultivars grown in Asia are susceptible to *Pgt*-TTKSK (Singh et al., 2008). Jin and Singh (2006) evaluated 450 cultivars and advanced breeding lines from the United States and found 84% of the hard red spring wheat, 52% of the hard red winter wheat, and 73% of the soft winter wheat to be susceptible to *Pgt*-TTKSK. However, much of this resistance can be attributed to *Sr24* and *Sr36* (Jin and Singh, 2006), to which races TTKST and TTTSK are virulent, respectively. Similarly, Fetch (2007) found the majority of the Canadian wheat cultivars to be susceptible to *Pgt*-TTKSK. Several genes have

been identified to be effective against *Pgt*-TTKSK (Jin et al., 2007). Most of these effective genes have been derived from alien relatives of wheat and many have not been used in breeding due to linkage drags (Singh et al., 2008).

One of the strategies to develop resistant cultivars to *Pgt*-TTKSK is to identify and introgress additional resistance genes from the wild relatives of wheat. Since *T. urartu* is the A-genome progenitor of wheat and *T. monococcum* is closely related to *T. urartu*, introgressions from these species to hexaploid wheat can be done with relative ease. Screening accessions of *T. monococcum* with multiple races has been used to postulate the presence of various resistance genes (The, 1973b). Three stem rust resistance genes have been identified and transferred from *T. monococcum*: *Sr21*, *Sr22*, and *Sr35* (Gerechter-Amitai et al., 1971; Kerber and Dyck, 1973; The, 1973a; The, 1973b; McIntosh et al., 1984). Races of *P. graminis* f. sp. *tritici* with virulence to *Sr21* are common (Huerta-Espino, 1992). A study of races from around the world failed to identify any virulent races to *Sr22* (Huerta-Espino, 1992). However, races with virulence to *Sr22* were reported in Israel (Gerechter-Amitai et al., 1971). Virulence to *Sr35* has been identified (Huerta-Espino, 1992). *Sr22* and *Sr35* have been shown to be effective to *Pgt*-TTKSK at both the seedling and adult plant stages but the effectiveness of *Sr21* in hexaploid wheat to *Pgt*-TTKSK was considered uncertain (Jin et al., 2007). The objective of this study was to identify *Pgt*-TTKSK resistance in *T. urartu* and *T. monococcum* germplasm.

Materials and methods

Available accessions (214 of *T. urartu* and 1061 of *T. monococcum*) were obtained from the United States Department of Agriculture National Small Grains Collection (Aberdeen, ID). The *T. monococcum* germplasm is divided into 847 accessions of *T. monococcum* subsp. *aegilopoides* (synonymous with wild einkorn, *T. aegilopoides,* and *T. boeoticum*) and 214 accessions of *T. monococcum* subsp. *monococcum* (cultivated einkorn). One accession classified as *T. monococcum* subsp. *aegilopoides*, PI 306526, is actually *T. dicoccoides* and was not included in the analyses (we obtained 1062 accessions from the National Small Grains Collection listed as *T. monococcum*). All accessions were screened with five races of *P. graminis* f. sp. *tritici* (*Pgt*, Table 4.1). Isolate 04KEN156 has previously been identified as race TTKSK (Jin and Singh, 2006; Jin et al., 2007; Wanyera et al., 2006) based on the North American differentials for *P. graminis* f. sp. *tritici* (Jin et al., 2008; Roelfs et al., 1993; Roelfs and Martens, 1988). Isolates of races TTTTF and TRTTF were used in this study because of their broad virulence to genes to which *Pgt*-TTKSK is avirulent (Table 4.1). Isolates of races QFCSC and MCCFC were selected because of their ability to differentiate among *T. monococcum* resistance genes *Sr21* and *Sr35* when used in combination with the other races.

Urediniospores of stem rust isolates in gelatin capsules stored at -80°C were heat-shocked at 45°C for 15 min, and placed in a rehydration chamber for 2 to 4 h maintained at 80% relative humidity by a KOH solution (Rowell, 1984). Procedures in inoculation,

incubation and disease assessment were performed as described previously (Jin et al., 2007). Susceptible controls (Chinese Spring and Rusty) and monogenic lines carrying *Sr21*, *Sr22*, and *Sr35* were inoculated with each race along with the test entries. Disease reactions were classified according to Stakman et al. (1962). Infection types '0', ';', '1', and '2' were considered low infection types characteristic of host resistance and pathogen avirulence. Infection types '3' and '4' were considered high infection types corresponding to susceptible accessions. When low and high infection types were present on the same leaf, the reaction was considered resistant. In each assay, six to ten plants were evaluated. When plants segregated for resistance within an accession, the accession was classified as heterogeneous. The combined reaction to all five races was determined for each accession where an accession was considered resistant to the combined races if the reaction to all five races was resistant. A total of 107 randomly selected *T. monococcum* accessions (10.1% of the total) were screened with races TTKSK, TTTTF, and TRTTF a second time to test the repeatability of scoring rust reactions. The frequency of misclassification of resistance was used as a measure of repeatability.

Frequencies of rust reactions (resistant, susceptible, and heterogeneous) to each of the five races and the combined reaction to all five races were calculated for *T. urartu* and *T. monococcum*. We calculated chi-square values in order to test the assumption of independence of reaction among the five races. Frequencies of rust reactions within the two *T. monococcum* subspecies were calculated. For *T. urartu*, 90.7% of the accessions were from either Turkey or Lebanon. Previous studies indicated that accessions from Turkey formed a distinct phylogenetic clade from accessions collected in Lebanon (Heun

et al., 2008). Therefore, we also calculated the percentage of resistant accessions from Turkey and Lebanon, separately. Chi-square values were also calculated to test for deviation in percent resistance between the wild and cultivated forms of *T. monococcum* and the Turkey and Lebanon collections of *T. urartu*.

We postulated the presence of *Sr21*, *Sr22*, and *Sr35* in *T. monococcum* accessions based upon known and observed reactions of the *Pgt* races on monogenic and digenic lines (The, 1973b; McIntosh et al., 1984). For *Sr21* postulations, we considered ITs '3-' or '3' to TTKSK as indicative of *Sr21* when resistance was also observed to race MCCFC. This exception to our protocol of classifying ITs '3-' and '3' as resistant instead of susceptible was made because other studies have shown that the reaction of *Pgt*-TTKSK to lines with *Sr21* can be intermediate (Chapter 2). We calculated the frequency of accessions postulated to possess known genes for both *T. monococcum* subsp. *aegilopoides* and *T. monococcum* subsp. *monococcum*.

Results

The screening data are available in Appendix II. The frequency and number of *T. monococcum* and *T. urartu* accessions resistant, susceptible, and heterogeneous to the five races and the races combined are displayed in Tables 4.2 and 4.3, respectively. A large proportion of the *T. monococcum* and *T. urartu* accessions were resistant to *Pgt*-TTKSK. Relatively few *T. monococcum* accessions were resistant to races TRTTF and TTTTF and no *T. urartu* accessions were resistant to these two races. We found a higher frequency of accessions resistant and heterogeneous to races TRTTF and TTTTF in *T. monococcum* subsp. *monococcum* relative to *T. monococcum* subsp. *aegilopoides* (Table 4.4). In contrast, a higher percentage of *T. monococcum* subsp. *aegilopoides* accessions were resistant to races TTKSK and MCCFC. *T. urartu* accessions collected in Lebanon were more often resistant to races TTKSK and MCCFC than those collected in Turkey (Tables 4.3, 4.4).

Associations of resistance to different races were significant as measured by the pair-wise comparisons except for the TRTTF-MCCFC and TTTTF-MCCFC race comparisons (Table 4.5). Overall, *T. monococcum* accessions resistant to one race were resistant to other races more often than expected under the assumption that resistance to the five races is independent. For *T. urartu*, associations were not significant (Table 4.5), indicating that independent race-specific genes likely confer resistance to races TTKSK, MCCFC, and QFCSC.

The infection types of three lines with known *T. monococcum* stem rust resistance genes are displayed in Table 4.6. A small subset of the accessions, their infection type patterns, and gene postulations are shown in Table 4.7. Some accessions displayed infection type patterns that could not be explained by the previously characterized resistance genes. The frequencies of postulated known genes are displayed in Table 4.8.

Out of 297 pair-wise comparisons of infection types, 14 comparisons were inconsistent resulting in a repeatability of 95.28%. Of those 14 comparisons, 9 were misclassified for *Pgt*-TTKSK with a '2+3' IT in one replication and a '3-' or '3' IT in the other replication. This variability is likely due to *Sr21* and was accounted for in the gene postulations ('3-' or '3' ITs to *Pgt*-TTKSK were considered as low for gene postulation). Excluding this variability, 5 comparisons were misclassified (98.32% repeatability). For these 5 misclassified comparisons, the ITs of the replications classified as resistant were '2+3', '23+Z', '2+3/123Z', or ';3+Z', indicating that misclassifications only occurred when the IT of the low (resistant) replication was relatively high. The infection type data used for the repeatability test are available in Appendix III.

Discussion

The slightly higher frequency of resistant accessions in *T. monococcum* subsp. *monococcum* relative to *T. monococcum* subsp. *aegilopoides* may be partly due to the presence of *Sr35* in accessions of *T. monococcum* subsp. *monococcum*. Accession G2919 (PI 428170) was used by P. L Dyck to introgress *Sr35* into hexaploid wheat (McIntosh et al., 1984). This accession was present in our germplasm and displayed a unique pattern of infection types: '0' to race TRTTF, '0' to race TTKSK, 'X-' LIF (mesothetic with low infection frequency) to race TTTTF, '4' to race QFCSC, and '4' or ';1' to race MCCFC (depending on the presence or absence of *Sr21*). This unique pattern of infection types was present in 21 accessions of *T. monococcum* subsp. *monococcum,* and this pattern was not found in accessions of *T. monococcum* subsp. *aegilopoides*. The higher proportion of resistance to races TTKSK and MCCFC in *T. monococcum* subsp. *aegilopoides* is likely due to a higher proportion of accessions carrying *Sr21* in this subspecies (Table 4.8).

A higher proportion of *T. urartu* accessions from Lebanon were resistant to races TTKSK and MCCFC compared to accessions from Turkey. The differences might be a result of the divergent evolutionary history known in this species from these two countries (Moghaddam et al., 2000; Heun et al., 2008). Identification of geographical areas where a higher proportion of collected landraces were resistant to stem rust has been used to prioritize further screening (Bonman et al., 2007). If this strategy is used for identifying stem rust resistance in *T. urartu*, screening of additional accessions from Lebanon, not Turkey, should be prioritized. However, relatively few *T. urartu* accessions

were screened in this study and additional screening of accessions could be beneficial, regardless of geographic origin.

Positive associations for resistance to different races in *T. monococcum* accessions suggest that resistance is usually effective against multiple races, when it is present. A large proportion of accessions exhibited resistance to races TTKSK and MCCFC. This resistance may be attributed to *Sr21*. Similarly, The (1973b) found the majority of *T. monococcum* accessions screened to possess *Sr21*. Though *Pgt*-TTKSK is known to produce moderately high infection types ('3' or higher) on *Sr21* in some hexaploid wheat lines, especially at low temperatures, a low infection type may be observed at the seedling stage in diploids. Several *T. monococcum* accessions displayed infection type patterns that could not be explained by *Sr21*, *Sr22*, or *Sr35* alone or in combination. We have selected a few of these accessions for developing segregating populations to investigate the genetics of *Pgt*-TTKSK resistance.

Triticum urartu has not been used as a source for the introgression of stem rust resistance genes. Therefore, the stem rust resistance observed is likely due to new genes. Accessions resistant to *Pgt*-TTKSK were often susceptible to other races used in this study, deviating from the pattern in *T. monococcum* where *Pgt*-TTKSK resistance is almost always associated with race MCCFC resistance, indicative of *Sr21*. Since we did not observe significant associations between the races, resistance to races TTKSK, QFCSC, and MCCFC is likely conferred by single race-specific resistance genes for each race.

Major-gene resistance introgressed from wild relatives of wheat has been an

effective source of genetic resistance to stem rust. New genes resistant to *Pgt*-TTKSK introgressed into adapted germplasm will aid breeders in developing resistant varieities. Screening the *T. monococcum* and *T. urartu* germplasm in this study resulted in the identification of new genes or alleles that provide resistance to *Pgt*-TTKSK. Genetic studies have been initiated to determine the number and allelic relationships of new resistance genes, to confirm our gene postulations, and to facilitate the mapping of *Sr21*, *Sr22*, *Sr35* and uncharacterized genes in diploid backgrounds.

Table 4.1. Races of *Puccinia graminis* f. sp. *tritici* used to screen *Triticum monococcum* germplasm

Race	Isolate	Virulence/Avirulence formula
TRTTF	06YEM34-1	5,6,7b,9a,9b,9d,9e,9g,10,11,17,21,30,36,38,McN,Tmp/8a,22,24,31,35
TTKSK	04KEN156/04	5,6,7b,8a,9a,9b,9d,9e,9g,10,11,17,30,31,38,McN/22,24,35,36,Tmp[a]
TTTTF	01MN84A-1-2	5,6,7b,8a,9a,9b,9d,9e,9g,10,11,17,21,30,36,McN,Tmp/22,24,31,35,38
QFCSC	03ND76C	5,8a,9a,9d,9g,10,17,21,35,McN/6,7b,9b,9e,11,22,24,31,30,36,38,Tmp
MCCFC	59KS19	5,7b,9g,10,17,35,McN,Tmp/6,8a,9a,9b,9d,9e,11,21,22,24,31,30,36,38

[a] *Sr21* is not included in the formula for *Pgt*-TTKSK.

Table 4.2. Number (and frequency) of *Triticum monococcum* accessions resistant, susceptible, and heterogeneous to five *Puccinia gramnis* f. sp. *tritici* races and the combined reaction to the five races

Accessions	Race	Total	Resistant		Susceptible		Heterogeneous	
T. monococcum	TRTTF	804	62	(7.7%)	724	(90.0%)	18	(2.2%)
subsp.	TTKSK	805	662	(82.2%)	109	(13.5%)	34	(4.2%)
aegilopoides	TTTTF	808	55	(6.8%)	741	(91.7%)	12	(1.5%)
	QFCSC	702	165	(23.5%)	523	(74.5%)	14	(2.0%)
	MCCFC	712	649	(91.1%)	42	(5.9%)	21	(2.9%)
	Combined	643	38	(5.9%)	594	(92.4%)	11	(1.7%)
T. monococcum	TRTTF	213	37	(17.4%)	161	(75.6%)	15	(7.0%)
subsp.	TTKSK	214	140	(65.4%)	52	(24.3%)	22	(10.3%)
monococcum	TTTTF	213	40	(18.8%)	157	(73.7%)	16	(7.5%)
	QFCSC	213	45	(21.1%)	162	(76.1%)	6	(2.8%)
	MCCFC	213	182	(85.4%)	25	(11.7%)	6	(2.8%)
	Combined	211	17	(8.1%)	186	(88.2%)	8	(3.8%)

Table 4.3. Number (and frequency) of *Triticum urartu* accessions resistant, susceptible, and heterogeneous to five *Puccinia gramnis* f. sp. *tritici* races and the combined reaction to the five races

Accessions	Race	Total	Resistant		Susceptible		Heterogeneous	
Lebanon	TRTTF	88	0	(0%)	88	(100%)	0	(0%)
T. urartu	TTKSK	87	86	(98.9%)	0	(0%)	1	(1.1%)
	TTTTF	92	0	(0%)	92	(100%)	0	(0%)
	QFCSC	87	1	(1.1%)	86	(98.9%)	0	(0%)
	MCCFC	86	48	(55.8%)	37	(43.0%)	1	(1.2%)
	Combined	78	0	(0%)	78	(100%)	0	(0%)
Turkey	TRTTF	81	0	(0%)	81	(100%)	0	(0%)
T. urartu	TTKSK	81	72	(88.9%)	4	(4.9%)	5	(6.2%)
	TTTTF	88	0	(0%)	88	(100%)	0	(0%)
	QFCSC	81	2	(2.5%)	78	(96.3%)	1	(1.2%)
	MCCFC	79	1	(1.3%)	76	(96.2%)	2	(2.5%)
	Combined	71	0	(0%)	71	(100%)	0	(0%)

Table 4.4. Association of rust reactions between the two subspecies of *T. monococcum* and two countries of origin of *T. urartu*

Species	Association between		Race	χ^2	Association Type [a]	*P* value
T. monococcum	Wild	Cultivated	TRTTF	20.38	WS/CR	1.41 E-4
	Wild	Cultivated	TTKSK	19.92	WR/CS	1.76 E-4
	Wild	Cultivated	TTTTF	32.75	WS/CR	3.64 E-7
	Wild	Cultivated	QFCSC	0.45	ns	0.93
	Wild	Cultivated	MCCFC	8.30	WR/CS	0.04
	Wild	Cultivated	Combined	2.30	ns	0.51
T. urartu	Lebanon	Turkey	TTKSK	8.15	LR/TS	0.043
	Lebanon	Turkey	QFCSC	0.80	ns	0.85
	Lebanon	Turkey	MCCFC	62.78	LR/TS	1.50 E-13

[a] For significant associations, the association type between classes (W, wild; C, cultivated; L, Lebanon; and T, Turkey) and either resistance (R) or susceptibility (S) are indicated. Symbol 'ns' indicates a non-significant association.

Table 4.5. Association of rust reactions among the five races in pair-wise comparisons as measured by chi-square values and probability

Species	Association between Race	Race	χ^2	Association Type [a]	*P* value
T. monococcum	TRTTF	TTKSK	15.90	+	0.0012
	TRTTF	TTTTF	554.10	+	8.99 E-120
	TRTTF	QFCSC	163.35	+	3.46 E-35
	TRTTF	MCCFC	1.70	ns	0.64
	TTKSK	TTTTF	17.79	+	4.86 E-4
	TTKSK	QFCSC	15.38	+	0.0015
	TTKSK	MCCFC	149.23	+	3.87 E-32
	TTTTF	QFCSC	131.90	+	2.11 E-28
	TTTTF	MCCFC	1.65	ns	0.65
	QFCSC	MCCFC	15.22	+	0.0016
T. urartu	TTKSK	QFCSC	0.28	ns	0.96
	TTKSK	MCCFC	2.29	ns	0.51
	QFCSC	MCCFC	4.35	ns	0.23

[a] For significant associations, '+' indicates a positive association among resistant accessions and '-' indicates a negative association among resistant accessions. Symbol 'ns' indicates a non-significant association.

Table 4.6. Infection type patterns of lines containing previously characterized *T. monococcum* stem rust resistance genes to *Puccinia gramnis* f. sp. *tritici* races used in this study

		Race					
Accession	**Background**	**TRTTF**	**TTKSK**	**TTTTF**	**QFCSC**	**MCCFC**	**Gene(s)**
CI 2433	diploid	3+	;1	3+	3+	;1	*Sr21*
G2919	diploid	0;	0	X- LIF[a]	4	;1	*Sr35* + *Sr21*
Sr22TB	hexaploid	;2-	2-	2	2-	1	*Sr22*

[a] 'X' indicates a mesothetic infection type with both high and low pustules. 'LIF' indicates low infection frequency.

Table 4.7. Infection type patterns and gene postulations for selected accessions of *T. monococcum*

	Race					Gene
Accession	**TRTTF**	**TTKSK**	**TTTTF**	**QFCSC**	**MCCFC**	**Postulation**
PI 272557	3+	4	4	4	4	Susceptible
PI 538720	3+	12+Z[a]	4	4	;1	*Sr21*
PI 554541	3+	2	3+	4	;1	*Sr21*
PI 330528	12-;	1;	12-;	;1	;1	*Sr22*
PI 428151	2+	2-	;1	;1	;1	*Sr22*
PI 272560	0;	0	X LIF[b]	4	4	*Sr35*
PI 277137	0;	0	X- LIF	4	4	*Sr35*
PI 306543	0	0	X- LIF	4	;1	*Sr21+Sr35*
PI 428175	0;	0;	X LIF	3+	;1	*Sr21+Sr35*
PI 538622	4	2-	4	4	4	-
PI 306540	;123Z	0;	;123Z	;1-	0	-

[a] 'Z' indicates the distribution of infection types across the leaf with the higher infection types occurring at the leaf base

[b] 'X' indicates a mesothetic infection type with both high and low pustules. 'LIF' indicates low infection frequency.

Table 4.8. Frequency of postulated stem rust resistance genes in *T. monococcum* germplasm

S[a]	Tot[e]	*Sr21*		*Sr22*		*Sr35*		*Sr21+Sr35*		Susceptible		Unknown	
A[b]	847	673	(79.5%)	52	(6.1%)	0	(0%)	0	(0%)	23	(2.7%)	99	(11.7%)
M[c]	214	128	(59.8%)	15	(7.0%)	6	(2.8%)	15	(7.0%)	15	(7.0%)	35	(16.4%)
T[d]	1061	801	(75.5%)	67	(6.3%)	6	(0.6%)	15	(1.4%)	38	(3.6%)	134	(12.6%)

[a] Species

[b] *Triticum monococcum* subsp. *aegilopoides*

[c] *Triticum monococcum* subsp. *monococcum*

[d] Total *Triticum monococcum*

[e] Total accessions

Chapter V

Genetics of resistance to race TTKSK of *Puccinia graminis* f. sp. *tritici* in *Triticum monococcum*

Summary

Race TTKSK (Ug99) of *Puccinia graminis* f. sp. *tritici* possesses virulence on several stem rust resistance genes commonly present in wheat cultivars grown worldwide. New variants detected in the race TTKS lineage further broadened the virulence spectrum. The identification of sources of genetic resistance to race TTKSK and its relatives is necessary to enable the deployment of resistant varieties. *Triticum monococcum*, an A-genome diploid wild and cultivated wheat, has been used as a source of stem rust resistance genes, including *Sr21*, *Sr22*, and *Sr35*. The objective of this study was to determine the genetic control and allelic relationships of resistance to race TTKSK in resistant *T. monococcum* accessions identified through evaluations at the seedling stage. F_2 progeny of 8 crosses between resistant and susceptible accessions and 13 crosses between resistant and resistant accessions of *T. monococcum* were evaluated with race TTKSK and often with North American races including races QFCSC, TTTTF, and MCCFC. For a selected population segregating for three genes conferring resistance to race TTKSK, $F_{2:3}$ progeny were evaluated with races TTKSK, QFCSC, and TTTTF. We detected at least two genes conferring resistance to race TTKSK that are different from *Sr21*, *Sr22*, and *Sr35*. One of the genes was effective to all races tested. The introgression of these genes into wheat will facilitate the development of varieties resistant to race TTKSK.

Introduction

Wheat stem rust, caused by the fungus *Puccinia graminis* f. sp. *tritici* (*Pgt*), is historically the most significant wheat disease. Emphasis in breeding wheat varieties for stem rust resistance and, in some locations, the removal of the alternate host, common barberry (*Berberis vulgaris* L.), of *Pgt* were successful in preventing significant epidemics of this disease in the United States and worldwide over the past several decades (Leonard, 2001).

In 1999, a race of *Pgt* was reported in Uganda with a unique combination of virulence making it capable of infecting the majority of the world's currently grown wheat cultivars (Pretorius et al., 2000). This race, commonly known as Ug99, was characterized as race TTKSK based upon it's reaction to the 20 standard North American differentials (*Pgt*-TTKSK; Jin et al., 2007; Jin et al., 2008). Seedling screening of wheat cultivars with *Pgt*-TTKSK found that 84% of the hard red spring wheat, 52% of the hard red winter wheat, and 73% of the soft winter wheat of United States cultivars and breeding lines and the majority of Canadian cultivars and breeding lines were susceptible (Jin and Singh, 2006; Fetch, 2007). Almost all cultivars from Asia screened in Kenya were susceptible (Singh et al., 2008).

In 2006, a variant of *Pgt*-TTKSK described as race TTKST was detected that possessed additional virulence to stem rust resistance gene *Sr24* (Jin et al., 2008). Many of the resistant varieties to *Pgt*-TTKSK in the United States possess *Sr24* (Jin and Singh, 2006). This gene is also widely deployed in many other countries, including Kenya. In

2007, race TTKST was widespread and varieties in Kenya with *Sr24* were no longer resistant to stem rust. In 2007, a second variant of Ug99, race TTTSK, was detected with virulence to *Sr36* (Jin et al., 2009). Unfortunately, many of the United States varieties resistant to *Pgt*-TTKSK in the soft red winter wheat market class possess *Sr36* (Jin and Singh, 2006). Race TTKSK has subsequently been found in Yemen and Iran (Nazari et al., 2009) and a variant, race PTKST, has been detected in South Africa (Pretorius et al., 2010).

In order to control *Pgt*-TTKSK and its variants, resistance genes will need to be combined and deployed in cultivars in order to provide more durable resistance. A number of designated resistance genes have been identified as effective to *Pgt*-TTKSK (Jin et al., 2007). Many of these resistance genes are derived from alien relatives of wheat and have not been used in breeding because of linkage drags (Singh et al., 2008).

Several stem rust resistance genes have previously been introgressed from *Triticum monococcum*, a wheat relative with a diploid A-genome (Gerechter-Amitai et al., 1971; Kerber and Dyck, 1973; The, 1973a; The, 1973b; McIntosh et al., 1984). One advantage of introgressing traits from *T. monococcum* as opposed to most other wheat relatives is that *T. aestivum* (bread wheat) chromatin recombines with introgressed chromatin from *T. monococcum*. This allows traits introgressed from *T. monococcum* to be backcrossed into wheat germplasm providing the opportunity to reduce the size of the alien chromatin and eliminate linkage to unwanted genes. Reduction of *T. monococcum* alien chromatin has recently been accomplished for an introgressed *T. monococcum* segment carrying *Sr22* (Olson et al., 2010).

We previously characterized 1061 *T. monococcum* accessions for resistance to stem rust including *Pgt*-TTKSK (Chapter 4). Preliminary gene postulations based upon infection type patterns allowed us to identify several accessions that likely possess new resistance to *Pgt*-TTKSK. The objective of this study was to determine the genetic control and allelic relationships of resistance to *Pgt*-TTKSK in resistant *T. monococcum* accessions.

Materials and methods

Accessions of *T. monococcum* used as parents in this study are listed in Table 5.1. The 21 crosses made among these accessions are listed in Table 5.2. All accessions belong to *T. monococcum* subsp. *monococcum* (cultivated einkorn) and were obtained from the United States Department of Agriculture National Small Grains Collection (Aberdeen, ID). Most of the infection type data of these accessions to various *Pgt* races used in this study were obtained from an earlier report (Chapter 4). F_2 progeny of the crosses were screened with selected *Pgt* races (Table 5.3). In addition to race TTKSK, the other four races listed in Table 5.3 were included in this study because of their ability to differentiate among the previously introgressed stem rust resistance genes from *T. monococcum* (*Sr21*, *Sr22*, and *Sr35*). Progeny of each cross were screened with particular races selected because of their specific avirulence phenotypes in order to discriminate among segregating genes. $F_{2:3}$ families were evaluated for the population derived from the cross PI 272557/PI 306540.

Urediniospores were retrieved from storage at -80°C and heat shocked at 45°C for 15 minutes. Spores were rehydrated by placing the capsules in an air-tight container at 80% humidity maintained by a KOH solution for 2 to 4 hours (Rowell, 1984). Urediniospores were then inoculated onto seedlings and plants were placed in dew chambers overnight as described previously (Jin et al., 2007). For each population of F_2 progeny analyzed, the parents of the population were included as controls. Infection types were classified on a 0 to 4 scale 14 days after inoculation as described by Stakman et al.

(1962, Figure 5.1). The biological repeatability of visually scoring infection types on *T. monococcum* leaves has been reported previously in our lab to be over 95% (Chapter 4). All visual scoring was performed by the same individual. Infection types '0' to '2' and 'X' or 'Z' were classified as low infection types indicating a resistant host and an avirulent isolate of *Pgt*. Infection types '3' and '4' were classified as high infection types indicating a susceptible host. In some populations it was possible to discriminate among resistant infection type classes. For each F_2 population, the number of susceptible and resistant progeny (or various classifications of resistance) were counted. For the $F_{2:3}$ population, 15-20 seedlings were scored for each family and two replications were performed for each race screened. Based upon the combined data from two replications, families were classified as homozygous resistant, segregating, or homozygous susceptible to each race. In each population, number of segregating resistance genes were predicted based upon chi-square goodness-of-fit tests.

Results and discussion

The presence of Sr21, Sr22, and Sr35 in the parental accessions

The segregation of resistance in accessions postulated to possess *Sr21*, *Sr22*, and/or *Sr35* is displayed in Table 5.4. CI 2433 was demonstrated to possess *Sr21* by The (1973b). Evaluating the F_2 progeny of the cross between CI 2433 and susceptible PI 272557 (C1) indicated the presence of a single dominant gene that provided resistance to *Pgt*-TTKSK (*Sr21*; Table 5.4).

An accession previously demonstrated to possess *Sr22* was not available to us. However, both PI 190945 and PI 428151-1 (a single plant selection of PI 428151) have infection type patterns identical to known lines with *Sr22* (The, 1973b; Kerber and Dyck 1973). Segregation of resistance in populations derived from crosses between these two accessions and susceptible PI 272557 to races TTKSK, TTTTF, and QFCSC (crosses C2 to C3) indicated the presence of a single dominant gene (Table 5.4). When the accessions were crossed with each other (cross C4), all progeny were resistant (Table 5.4) indicating that the accessions have the same gene. Two genes segregated for resistance to *Pgt*-TTKSK (avirulent on *Sr21*, Chapter 2) in progeny of crosses of CI 2433 (*Sr21*) with PI 428151-1 (C5) and PI 190945 (C6). When tested with races QFCSC and TTTTF (both virulent on *Sr21*), the F_2 populations segregated as a single gene. These data indicate that resistance to races QFCSC and TTTTF in PI 190945 and PI 428151-1 is different from *Sr21*. Similarly, two genes segregated for resistance in the cross (C8) between PI 428151-1 and PI 272560 (postulated to possess *Sr35*), indicating that the resistance in PI

428151-1 is independent from *Sr35*. None of the evidence available to us indicates that the gene in PI 190945 and PI 428151-1 is not *Sr22*.

The source of *Sr35*, G2919, was demonstrated to also possess *Sr21* by McIntosh et al. (1984). As the majority of *T. monococcum* accessions possess *Sr21* (Chapter 4; The, 1973b), it is not surprising that an accession with *Sr35* also carries *Sr21*. Accession PI 272560 appeared to possess *Sr35* and not *Sr21* (Table 5.3). Unfortunately, crosses to PI272560 were rarely successful. However, we did establish that resistance in PI272560 to races TTKSK and TTTTF is inherited as a single dominant gene (C7, Table 5.4) confirming that *Sr35* is present alone in this line. Two genes segregated for resistance in G2919 to TTKSK (*Sr21* and *Sr35*; C9; Table 5.4). Accession DV92 showed identical infection types and race specificity as G2919, indicating that DV92 also possessed *Sr21* and *Sr35*. Examining segregation of progeny between DV92 and susceptible PI 272557 (C10) indicated the presence of two genes providing resistance to race TTKSK (*Sr21* and *Sr35*), one to race TTTTF (*Sr35*), and one to race MCCFC (*Sr21*). The presence of *Sr21* in DV92 was also confirmed in the cross between DV92 and CI 2433 (C11). Susceptible progeny were not observed in the cross between G2919 and DV92 (C12) when tested with the three races, indicating that the accessions possess the same genes.

In all population by race combinations, the number of segregating genes matched our expectations based upon gene postulations. Genes *Sr21*, *Sr22*, and *Sr35* segregated independently as expected since they are located on different chromosomes (2AL, 7AL, and 3AL, respectively; The, 1973b; Kerber and Dyck, 1973; McIntosh et al., 1984). Confirming the postulations of *Sr21*, *Sr22*, and *Sr35* is an essential prerequisite for

examining the genetics of resistance in accessions postulated to possess new resistance genes.

Resistance in PI 277131-2

Accession PI 277131-2 is a single plant selection from PI 277131 that was postulated to possess new resistance to race TTKSK. The infection type pattern exhibited by PI 277131-2 cannot be explained by the presence of *Sr21*, *Sr22*, or *Sr35* alone or in combination (Table 5.1). The high infection type conferred by race TTTTF on PI 277131-2 indicates that PI 277131-2 does not possess *Sr35*. The high infection types conferred by races TTTTF and TRTTF indicate that PI 277131-2 does not possess *Sr22*. The infection type pattern does not provide enough information to determine whether or not PI 277131-2 possesses *Sr21*. Two genes resistant to race TTKSK segregated in the F_2 progeny of the cross between PI 277131-2 and susceptible PI 272557 (C13; Table 5.5).

In order to determine if one of the genes in PI 277131-2 is *Sr21*, F_2 progeny from a cross to CI 2433 (*Sr21*; C14) were examined. One gene segregated for resistance to race QFCSC (virulent on *Sr21*) and no susceptible progeny were identified when screening with race MCCFC (avirulent on *Sr21*). These data suggest that one of the genes for resistance to race TTKSK in PI 277131-2 is *Sr21* and that the other gene is likely new because it is susceptible to race TTTTF, unlike *Sr22* and *Sr35*. To determine the allelic relationship between the new gene and *Sr22* and *Sr35*, crosses were made to PI 190945 (*Sr22*; C15), G2919 (*Sr21* and *Sr35*; C16), and DV92 (*Sr21* and *Sr35*; C17). No F_2 progeny were found to be susceptible from the cross with PI 190945 (*Sr22*; C15). This

result is likely due to the small population size sampled. Segregation of resistance to *Pgt*-TTKSK between PI 277131-2 and both DV92 and G2919 (C16, C17) indicated the presence of three distinct classes of resistant phenotypes that did not deviate significantly from a 12:3:1 ratio. This is consistent with the expectation that *Sr21* was fixed in these populations with *Sr35* and the new gene segregating. These data indicate that the new gene is independent of *Sr35*. The '0' to '0;' low infection type of *Pgt*-TTKSK on *Sr35* facilitated identification of lines without *Sr35*, but still resistant (with *Sr21* and sometimes the new gene).

Resistance in PI 306540

Accession PI 306540 was postulated to possess new resistance to race TTKSK because of its unique infection type pattern to the races screened (Table 5.1). PI 306540 is resistant to all races screened, but the mesothetic reactions observed with race TRTTF was not consistent with infection types produced by accessions with *Sr22* or *Sr35* (The, 1973b; Kerber and Dyck, 1973; Table 5.1). Analysis of $F_{2:3}$ progeny derived from the cross between PI 306540 and susceptible PI 272557 (C18) indicated segregation for 3 genes resistant to race TTKSK, 2 genes resistant to race QFCSC, and 1 gene resistant to race TTTTF (Table 5.6). Selected plants from homozygous families of this population and the parents inoculated with races TTTTF and QFCSC are displayed in Figure 5.2. Family 42 possesses a gene that mediates a ';13Z' infection type to races TTTTF and QFCSC (the middle of the leaves are displayed in Figure 5.2). Family 7 possesses a gene that mediates a '2' infection type to race QFCSC, but not race TTTTF. Family 49

possesses both genes resulting in the parental infection type to both races TTTTF and QFCSC.

Crossing of PI 306540 with CI 2433 (*Sr21*; C19) indicated that one of the genes that confers resistance to *Pgt*-TTKSK in PI 306540 is likely *Sr21* (Table 5.6). The resistance genes present in PI 306540 to races QFCSC and TTTTF are independent of *Sr21* since these races are virulent on *Sr21*. The presence of only 2 genes resistant to race QFCSC in PI 306540 and one gene resistant to race TTTTF is consistent with the hypothesis that one of the three genes resistant to *Pgt*-TTKSK in PI 306540 is *Sr21* since races QFCSC and TTTTF are virulent on *Sr21*. Examining progeny of the cross between PI 428151-1 (*Sr22*) and PI 306540 (C20) indicated that resistance to races TTTTF and QFCSC in PI 306540 is independent of *Sr22*. The sample size of plants observed was not sufficient enough to test whether or not resistance to *Pgt*-TTKSK is conferred by loci independent of *Sr22*. Progeny of the cross between PI 306540 and DV92 (*Sr21* and *Sr35*) segregated for the '0' to '0;' low infection type, indicative of *Sr35*, demonstrating the independence of resistance in PI 306540 to *Pgt*-TTKSK from *Sr35*.

In summary, of the three genes resistant to *Pgt*-TTKSK in PI 306540, (1) one is *Sr21*, (2) a new gene is present that confers a ';13Z' infection type and (3) a second new gene is present that confers a '2' infection type. The ';13Z' gene appears to display resistance to all races screened. Based upon race-specificity and infection type, the second new gene with the '2' infection type could be the same as the new gene identified in PI 277131-2. Crossing PI 277131-2 with PI 306540 and evaluating a large number of

progeny with race QFCSC may determine if resistance in the two accessions is independent.

Overall, we described at least two new stem rust resistance genes present in *T. monococcum* germplasm. We have initiated experiments to map the new resistance genes to facilitate the introgression of small segments of *T. monococcum* possessing resistance to *Pgt*-TTKSK into wheat. This study is valuable in increasing the potential 'toolbox' of resistance genes available to breeders for pyramiding multiple resistance genes into elite breeding lines in order to obtain durable resistance to stem rust.

Table 5.1. *Triticum monococcum* accessions used as parents in crosses and their infection types to selected races of *Puccinia graminis* f. sp. *tritici*

Accession	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Postulated gene(s)
PI 272557	3+	4	4	4	4	Susceptible parent
CI 2433	3+	2+	3+	4	;1	*Sr21*
PI 190945	1;	1	2-;	;1-	;1	*Sr22*
PI 428151-1	2+	2-	2	;1	;1	*Sr22*
PI 272560	0;	0	X LIF[a]	4	4	*Sr35*
G2919	0	0	X- LIF	4	;1	*Sr21,Sr35*
DV92	0	0;	X LIF	3+	1	*Sr21,Sr35*
PI 277131-2	3+	0;	3+	;12-	;	new
PI 306540	;13Z[b]	0;	;13Z	;1-	0	new

[a] 'X' indicates a mesothetic infection type with both high and low pustules. 'LIF' indicates low infection frequency.

[b] 'Z' indicates the distribution of infection types across the leaf with the higher infection types occurring at the leaf base.

Table 5.2. List of crosses made among *Triticum monococcum* accessions

Cross number	Parent 1	Parent 2
C1	PI 272557	CI 2433
C2	PI 272557	PI 428151-1
C3	PI 272557	PI 190945
C4	PI 428151-1	PI 190945
C5	CI 2433	PI 428151-1
C6	CI 2433	PI 190945
C7	PI 272557	PI 272560
C8	PI 428151-1	PI 272560
C9	PI 272557	G2919
C10	PI 272557	DV92
C11	CI 2433	DV92
C12	G2919	DV92
C13	PI 272557	PI 277131-2
C14	CI 2433	PI 277131-2
C15	PI 190945	PI 277131-2
C16	G2919	PI 277131-2
C17	DV92	PI 277131-2
C18	PI 272557	PI 306540
C19	CI 2433	PI 306540
C20	PI 428151-1	PI 306540
C21	DV92	PI 306540

Table 5.3. Races of *Puccinia graminis* f. sp. *tritici* used to screen progeny of *Triticum monococcum* crosses

Race	Isolate	Virulence/Avirulence formula
TRTTF	06YEM34-1	5,6,7b,9a,9b,9d,9e,9g,10,11,17,21,30,36,38,McN,Tmp/ 8a,22,24,31,35
TTKSK [a]	04KEN156/04	5,6,7b,8a,9a,9b,9d,9e,9g,10,11,17,30,31,38,McN/ 22,24,35,36,Tmp
TTTTF	01MN84A-1-2	5,6,7b,8a,9a,9b,9d,9e,9g,10,11,17,21,30,36,McN/ 22,24,31,35,38
QFCSC	03ND76C	5,8a,9a,9d,9g,10,17,21,35,McN/ 6,7b,9e,9b,11,22,24,31,30,36,38,Tmp
MCCFC	59KS19	5,7b,9g,10,17,35,McN,Tmp/ 6,8a,9a,9d,9e,9b,11,21,22,24,31,30,36,38

[a] *Sr21* is not included in the formula for *Pgt*-TTKSK.

Table 5.4. Segregation of resistance in *T. monococcum* F_2 progeny segregating for *Sr21*, *Sr22*, and/or *Sr35*

Cross	Race	R1[a]	R2[b]	Suscep.[c]	Expected Ratio	χ^2	*P*	Segregating Genes	Fixed Genes
C1	TTKSK	102	-	39	3:1	0.53	0.47	Sr21	-
C2	TTKSK	111	-	38	3:1	0.02	0.89	Sr22	-
C2	TTTTF	50	-	19	3:1	0.24	0.63	Sr22	-
C2	QFCSC	94	-	37	3:1	0.74	0.39	Sr22	-
C3	TTKSK	141	-	52	3:1	0.39	0.53	Sr22	-
C3	TTTTF	140	-	43	3:1	0.22	0.64	Sr22	-
C3	QFCSC	107	-	37	3:1	0.04	0.85	Sr22	-
C4	TTKSK	62	-	0	-	-	-	-	Sr22
C4	TTTTF	160	-	0	-	-	-	-	Sr22
C4	QFCSC	207	-	0	-	-	-	-	Sr22
C5	TTKSK	52	-	4	15:1	0.08	0.78	Sr21,Sr22	-
C5	TTTTF	16	-	6	3:1	0.14	0.71	Sr22	-
C5	QFCSC	62	-	28	3:1	1.79	0.18	Sr22	-
C6	TTKSK	14	-	1	15:1	4.44E-03	0.95	Sr21,Sr22	-
C6	TTTTF	44	-	18	3:1	0.54	0.46	Sr22	-
C7	TTKSK	68	-	20	3:1	0.24	0.62	Sr35	-
C7	TTTTF	66	-	21	3:1	0.03	0.85	Sr35	-
C8	TTKSK	39	13	3	12:3:1	0.88	0.64	Sr22,Sr35	-
C9	TTKSK	49	-	2	15:1	0.47	0.49	Sr21,Sr35	-
C10	TTKSK	131	27	14	12:3:1	1.87	0.39	Sr21,Sr35	-
C10	TTTTF	110	-	31	3:1	0.68	0.41	Sr35	-
C10	MCCFC	93	-	31	3:1	0	1.00	Sr21	-
C11	TTKSK	63	15	-	3:1	1.38	0.24	Sr35	Sr21
C11	TTTTF	57	-	15	3:1	0.67	0.41	Sr35	-
C11	MCCFC	78	-	0	-	-	-	-	Sr21
C12	TTKSK	67	-	-	-	-	-	-	Sr35
C12	TTTTF	75	-	-	-	-	-	-	Sr35
C12	MCCFC	70	-	-	-	-	-	-	Sr21

[a] Resistant type 1. By default, resistant plants were classified as type 1.

[b] Resistant type 2. When distinct categories of resistant plants were observed, the resistance was classified according to different types.

[c] Susceptible.

Table 5.5. Segregation of resistance in *T. monococcum* F_2 progeny derived from crosses with PI 277131-2

Cross	Race	R1[a]	R2[b]	R3	Susceptible	Expected Ratio	χ^2	*P*	Segregating Genes
C13	TTKSK	102	25	-	14	12:3:1	3.26	0.2	2 genes
C14	TTKSK	280	-	-	-	-	-	-	-
C14	TTTTF	-	-	-	89	-	-	-	-
C14	QFCSC	106	-	-	40	3:1	0.45	0.5	1 gene
C14	MCCFC	213	-	-	-	-	-	-	-
C15	TTKSK	206	-	-	-	63:1	13.73	2.10E-04	-
C16	TTKSK	89	16	7	-	12:3:1	1.49	0.48	*Sr35*, 1 gene
C17	TTKSK	80	27	5	-	12:3:1	2.48	0.29	*Sr35*, 1 gene

[a] Resistant type 1. By default, resistant plants were classified as type 1.

[b] Resistant type 2. When distinct categories of resistant plants were observed, the resistance was classified according to different types.

Table 5.6. Segregation of resistance in *T. monococcum* progeny derived from crosses with PI 306540

Cross	Race	G[a]	R1[b]	R2(F_2)/ Seg.(F_3)[c]	Susceptible	Expected Ratio	χ^2	*P*	Segregating Genes
C18	TTKSK	F_3	42	28	0	37:26:1	1.16	0.56	3 genes
C18	TTTTF	F_3	12	40	18	1:2:1	2.46	0.29	1 gene
C18	QFCSC	F_3	29	38	5	7:8:1	0.37	0.83	2 genes
C19	TTKSK	F_2	395	-	0	-	-	-	-
C19	TTTTF	F_2	80	-	25	3:1	0.08	0.78	1 gene
C19	QFCSC	F_2	142	-	9	15:1	0.02	0.88	2 genes
C20	TTKSK	F_2	453	-	0	-	-	-	-
C20	TTTTF	F_2	63	15	4	12:3:1	0.3	0.86	*Sr22*, 1 gene
C20	QFCSC	F_2	183	-	5	63:1	1.47	0.23	*Sr22*, 2 genes
C21	TTKSK	F_2	181	59	-	3:1	0.02	0.88	*Sr35*

[a] Generation

[b] Resistant type 1. By default, resistant plants were classified as type 1. Homozygous resistant F_3 families were also recorded as resistant type 1.

[c] Resistant type 2. When distinct categories of resistant plants were observed, the resistance was classified according to different types. Segregating F_3 families were included in the same column as R2.

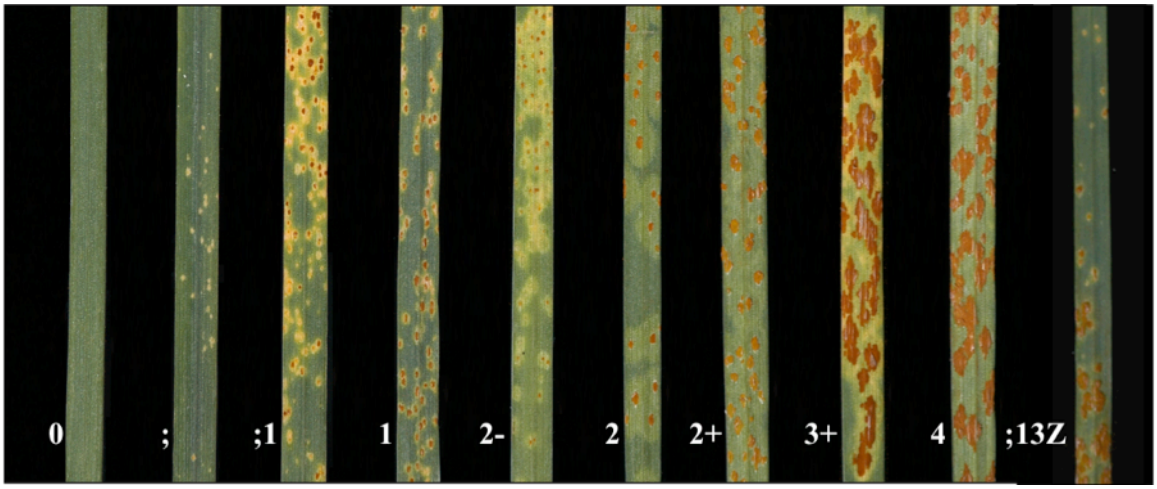

Figure 5.1. *Puccinia graminis* f. sp. *tritici* infection types on seedling *T. monococcum* leaves

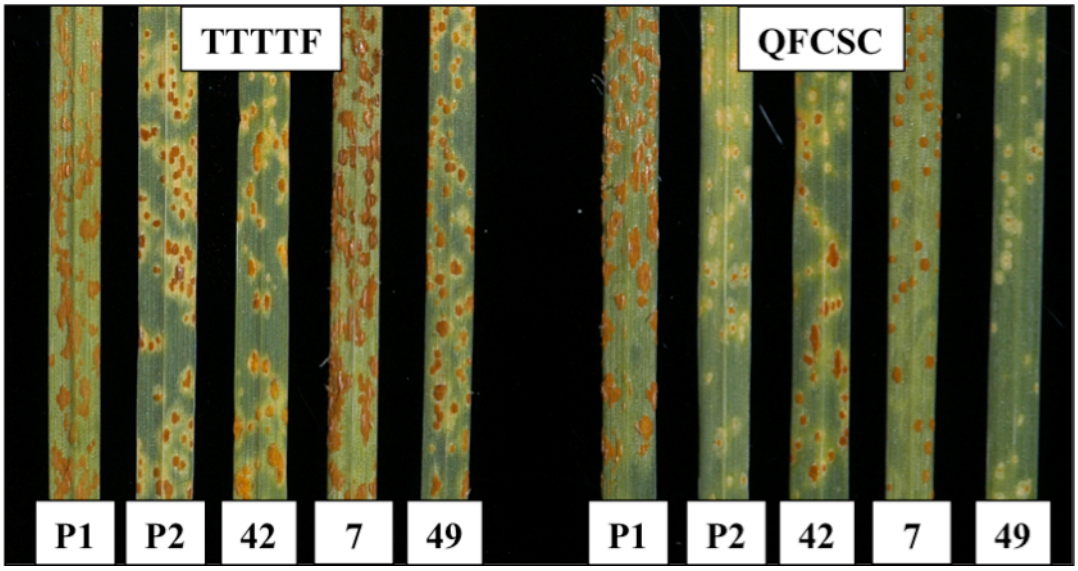

Figure 5.2. Infection types of selected homozygous PI 272557/PI 306540 F_3 families and parents (P1 is PI 272557, P2 is PI 306540) inoculated with races TTTTF and QFCSC of *Puccinia graminis* f. sp. *tritici*

Chapter VI

Sources of resistance to *Puccinia graminis* f. sp. *tritici* race Ug99 in spring wheat germplasm

Summary

Wheat stem rust (*Puccinia graminis* Pers.:Pers. f. sp. *tritici* Eriks & E. Henn.) race TTKSK (Ug99) with virulence to the majority of the world's wheat (*Triticum aestivum* L.) varieties has spread from Uganda throughout eastern Africa, Yemen, and Iran. The identification and spread of variants of race TTKSK with virulence to additional stem rust resistance genes has warned breeders and pathologists of the danger of deploying major resistance genes singly. In order to protect wheat from this rapidly spreading and adapting pathogen, multiple resistance genes are needed, preferably from relatively well-adapted germplasm. Preliminary screening of over 700 older spring wheat breeding lines and cultivars identified 88 accessions with field resistance to Ug99. We included these resistant accessions in the stem rust screening nursery in Njoro, Kenya for three seasons. The accessions were also screened with a bulk of North American isolates of *P. graminis* f. sp. *tritici* (*Pgt*) in the field in St. Paul, Minnesota. In order to further characterize the resistance in these accessions, we obtained seedling phenotypes for ten races of *Pgt*, including two races from the race TTKSK complex. This phenotyping led to the identification of accessions with either adult-plant or all-stage resistance to race TTKSK and often North American races of *Pgt* as well. Resistance to Ug99 identified in these accessions can be introgressed into current breeding germplasm.

Introduction

Wheat stem rust, caused by *Puccinia graminis* Pers.:Pers f. sp. *tritici* Eriks. & E. Henn. (*Pgt*), has historically been a major wheat (*Triticum aestivum* L.) yield-limiting factor. In the United States, epidemics of stem rust caused yield losses exceeding 50% statewide in North Dakota and Minnesota in 1935 and exceeding 40% in North Dakota in 1954 (Roelfs, 1978). Intensive efforts in breeding for stem rust resistance and the removal of the alternate host of stem rust in some locations led to the successful control of this disease both in the United States and worldwide for the past several decades (Leonard, 2001).

A race of stem rust was reported in Uganda in 1999 with a unique virulence profile that caused scientists to suspect that it could be a major threat to wheat production (Pretorius et al., 2000). This race, commonly referred to as Ug99, was characterized as race TTKSK according to the standard North American differentials (*Pgt*-TTKSK; Jin et al., 2007; Jin et al., 2008). With epidemics of stem rust caused by *Pgt*-TTKSK becoming frequent in Kenya starting in the mid 2000's, *Pgt*-TTKSK received acknowledgement as a major threat to global wheat production. Screening of currently grown cultivars from Asia indicated that nearly all were susceptible (Singh et al., 2008), and the majority of cultivars were susceptible in Canada and the United States, including 84% of the hard red spring wheat cultivars in the United States grown where stem rust epidemics have historically been most significant (Roelfs, 1978; Jin and Singh 2006; Fetch 2007).

The subsequent spread of *Pgt*-TTKSK to Yemen in 2006 and Iran in 2007, and the detection of *Pgt*-TTKSK-related races in South Africa in 2010 suggest that *Pgt*-TTKSK may soon reach major wheat production areas in other countries (Nazari et al., 2008; Pretorius et al., 2010). The detection of variants of *Pgt*-TTKSK with additional virulences on wheat stem rust resistance genes *Sr24* and *Sr36* indicates that the *Pgt*-TTKSK complex is more virulent than originally described (Jin et al., 2008; Jin et al., 2009). The variant of *Pgt*-TTKSK with virulence on *Sr24*, race TTKST, rendered susceptible a previously resistant variety that was widely deployed in Kenya. Much of the resistance to *Pgt*-TTKSK in current cultivars in the United States is conferred by *Sr24* and *Sr36* (Jin and Singh, 2006). Detection of these variants of *Pgt*-TTKSK and previous experiences in breeding resistant varieties of small grains to rusts suggest that multiple effective resistance genes will need to be combined into single cultivars in order for durable resistance to be achieved (Schafer and Roelfs, 1985; Kolmer et al., 1991).

Several resistance genes have been identified that are effective against *Pgt*-TTKSK (Jin et al., 2007). However, many of these genes are of partial effect, are race-specific, and are linked to undesirable traits on alien chromatin. Resistance available in adapted germplasm is conferred by relatively few resistance genes including *Sr25*, *SrTmp*, and *Sr1A.1R* (Jin and Singh, 2006; Singh et al., 2008; Njau et al., 2010). Additionally a few varieties and breeding lines exist with unknown resistance genes including sources possessing adult plant resistance (Njau et al., 2010). Given the few available sources of resistance to Ug99, their low frequency in adapted germplasm, and the rapid adaptation of Ug99 to previously effective resistance genes, it is essential to identify and

characterize multiple sources of resistance. In order to provide breeders with additional sources of resistance to *Pgt*-TTKSK in cultivated spring wheat, we screened over 700 older spring wheat breeding lines and cultivars for resistance in the field in Kenya in 2005. 88 accessions were identified as providing resistance to Ug99. Our objective was to characterize the stem rust resistance of the 88 accessions by screening with multiple isolates of *Pgt* at both seedling and adult plant stages.

Materials and methods

Greenhouse seedling screening

Seedling screening was performed with 8 North American races of *Pgt* and two isolates of *Pgt* from Kenya (Table 6.1). Isolate 04KEN156/04 is race TTKSK (Ug99) and isolate 06KEN19-V-3 is race TTKST, the *Pgt*-TTKSK variant with additional virulence to *Sr24* (Jin et al., 2007; Jin et al., 2008). All isolates were purified from single-pustules, increased in isolation, and stored at -80°C. The 88 lines used in this study were obtained from the United States Department of Agriculture National Small Grains Collection (Aberdeen, ID). The accessions are listed in Table 5.2 and pedigree, source, and descriptive information can be found online at http://www.ars-grin.gov/npgs/index.html (22 June 2010). A selection of susceptible line LMPG, LMPG-6, was used as a control in all evaluations (Knott, 1990). Seedling screening with Kenyan isolates of *Pgt* was conducted only during the winter months of December, January, and February as a precaution to prevent the escape of these cultures.

Pgt urediniospores were retrieved form -80°C storage, heat-shocked at 45°C for 15 minutes, placed in a rehydration chamber for 2 to 4 hours maintained at 80% relative humidity by a KOH solution (Rowell, 1984), and mixed with a light weight mineral oil (Soltrol 70, ConocoPhillips Inc., Houston, TX) in preparation for inoculation. Spores were inoculated onto the primary leaves of seedling *T. aestivum* plants 7 to 9 days following planting. The plants were placed under a fume hood to allow the oil to evaporate for approximately 30 minutes. The dried leaves were placed into a dark dew

chamber for 14 hours at 18°C, followed by an additional 3 to 4 hours with fluorescent light. The plants were then placed in a greenhouse maintained at 18±2°C with a photoperiod of 16 hours. Infection types were recorded on a '0' to '4' scale 14 days post inoculation after Stakman et al. (1962). 'X' was used to denote mesothetic reactions (all infection types occurring on the same leaf). 'C' was used to denote extensive chlorosis associated with *Pgt* infection. 'N' was used to denote extensive necrosis. When an accession displayed a relatively low frequency of pustules of stem rust, the infection type was recorded followed by 'LIF' (low infection frequency). '+' and '-' symbols were sometimes used to describe relative size of pustules for each infection type classification. Five to six plants of each accession were evaluated for each inoculation with a unique *Pgt* isolate. When accessions were heterogeneous for infection types, the infection type was recorded as the most frequent infection type, followed by a '/', followed by the next most frequent infection type. For the North American *Pgt* isolates, the experiments were repeated. For 04KEN156/04, four replicates were conducted. A set of the standard North American stem rust differentials were included in each inoculation with each isolate.

Field adult-plant screening

In order to evaluate field resistance at the adult plant stage for the 88 accessions both to Kenyan and domestic *Pgt* isolates, field trials were conducted both at Saint Paul, Minnesota, USA and Njoro, Kenya. The lines were grown in Njoro from June through October in three seasons (2005-2007). In Saint Paul, the lines were grown from April to August in 2006.

In Saint Paul, the 88 accessions were included as part of the stem and leaf rust (*Puccinia triticina* Eriks.) nursery used for screening United States spring wheat germplasm with domestic stem and leaf rust isolates. The field plots consisted of 2 m long single row plots. Plots were separated by 20 cm with 2 m alleys. Alleys were alternatively planted with winter wheat or a mixture of varieties selected for their susceptibility to stem and/or leaf rust (Thatcher, Morocco, LMPG-6, and Rusty) to serve as spreaders. Spreader rows were planted 1 to 2 weeks before the experimental plots. Spreader and winter wheat rows were planted perpendicular to the experimental plots. In Njoro, the accessions were included as a part of an international nursery established by the Kenyan Agricultural Research Institute (nursery described in more detail in Jin et al., 2007). The plots consisted of single 2 m rows in 2005 and two 1 m rows in 2006 and 2007. Spreader rows of Ug99-susceptible cultivars Chozi and Duma were planted perpendicular to the experimental plots.

Epidemics of stem rust were initiated at Saint Paul by the inoculation of spreader rows. A water suspension of bulked urediniospores of North American *Pgt* races QFCSC, TPMKC, RKQQC, RCRSC, QTHJC, and MCCFC was inoculated onto spreader rows by injection into the elongating stems using a hypodermic needle. A stem in the spreader row was injected approximately every 2 m on each side of the speader row. Also, a light mineral oil suspension of the bulked *Pgt* races was inoculated onto the spreader rows using an Ulva+ sprayer (Micron Sprayers Ltd, Bromyard, UK). Specific methods of inoculating spreader rows were followed as described in Jin et al. (1994). These inoculations were performed when plants in the spreader row were jointing. In Njoro,

urediniospores were collected from experimental plots of the variety Duma (possesses *Sr31*; *Pgt*-TTKSK and variants are the only known stem rust races virulent to *Sr31*). The urediniospores were mixed with talc powder and dusted onto the spreader rows. Surveys of *Pgt* races present in the Njoro nursery indicated that TTKSK was the only described race in 2005, race TTKSK predominated in 2006 with race TTKST present at a low frequency, and both races TTKSK and TTKST predominated in 2007 with trace levels of race TTTSK being detected (Jin et al., 2008, Jin et al., 2009).

Infection response was classified for each line according to size of pustules and amount of chlorosis and necrosis (Roelfs et al., 1992). Infection response categories included resistant (R), moderately resistant (MR), moderately susceptible (MS), and susceptible (S). If a line displayed multiple infection responses to stem rust, they were all recorded (example: MR-MS). Severity of stem rust was visually scored on the 0 to 100 modified Cobb scale (Peterson et al., 1948). When lines were observed to be heterogeneous for infection response and/or severity a '/' was used to separate readings from different plants of the same line.

Results

The 88 accessions displayed a wide range of seedling infection types to *Pgt*-TTKSK (Table 6.2). Several accessions displayed '3' to '4' infection types indicating that those lines possess only adult plant resistance to *Pgt*-TTKSK. Several accessions were observed to be heterogeneous in seedling infection types. Nearly all of the accessions remained resistant across multiple years of field screening in Kenya (Table 6.2). These resistant responses are in sharp contrast with the high severity and susceptible infection responses observed on LMPG-6 throughout the three seasons. PI 234234 displayed very good resistance in 2005, but was read at 70 S in 2007. We are unsure of the reason for this inconsistency. In 2007 the infection responses and severities were less susceptible/severe than in previous years. This is likely due to the relative late planting date for these accessions during 2007.

Screening of the 88 accessions with 8 North American *Pgt* isolates at the seedling stage resulted in a broad range of infection types (Table 6.2, Appendix IV). Infection types remained consistent across the two replications for each race. All of the accessions were resistant in the field except PI 254138. A few accessions were resistant in the field, but susceptible to many of the *Pgt* isolates at the seedling stage. An extreme example of this was CI 12499, which was susceptible to all *Pgt* isolates except BCCBC (not present in field nursery) at the seedling stage, but resistant at the adult plant stage.

Discussion

Screening of over 700 accessions of spring wheat resulted in the identification of 88 with field resistance to Ug99. Though the frequency of resistance to Ug99 in the initial germplasm is low, the number of resistant lines is promising for the identification of new resistance and introgression of resistance into currently grown cultivars. Nearly all of the lines that were identified as resistant in the field to Ug99 were also resistant in the field to North American isolates of *Pgt* (Table 6.2, Appendix IV). This suggests that either the resistance effective to Ug99 also confers resistance to North American isolates or that the accessions contain multiple resistance genes that confer resistance to a broad range of isolates. Regardless of the mechanism, the characterization of stem rust resistance in these accessions indicates that they are valuable for providing resistance to Ug99 as well as North American isolates of *Pgt*.

It has been proposed that lines that are susceptible at the seedling stage, but resistant at the adult plant stage possess resistance that will be durable (Singh et al., 2008). Several sources of resistance have been identified in CIMMYT wheat breeding germplasm that are susceptible to *Pgt*-TTKSK at the seedling stage but exhibit a high level of resistance at the adult plant stage (Njau et al., 2010). These sources are being used extensively as parents of breeding populations for use in east Africa and the Middle East (Singh et al., 2008). We identified 16 lines that are susceptible to races TTKSK and TTKST at the seedling stage (‘3’ to ‘4’ infection types), yet resistant in the field (Table 6.2). Ten of these lines are from hard red spring wheat breeding programs in the North

American northern Great Plains including six from the University of Minnesota. Many of the lines with adult plant resistance have Thatcher wheat in their pedigrees, and at least two (CI 11781 and CI 12040) are derived from line H-44, which possesses the adult plant resistance gene *Sr2*. These lines are supposed to be the source of adult plant resistance observed in older CIMMYT wheat cultivars that were deployed widely as part of the Green Revolution (Singh et al., 2008). Further studies will be necessary to determine the genetics of stem rust resistance in these accessions. It is possible that adult plant resistance independent of 'Thatcher' or *Sr2* exists in this germplasm.

The majority of the accessions characterized were resistant at both seedling and adult plant stages to both Kenyan and North American isolates of *Pgt*. Likely, race-specific major genes such as *Sr6* and *Sr36* are contributing to the observed seedling resistance to North American isolates of *Pgt* in this germplasm (Tsilo et al., 2008; Tsilo et al., 2009). However, few known sources of seedling resistance to *Pgt*-TTKSK (Jin et al., 2007) and their limited use in cultivars (Jin and Singh, 2006) suggest that there could be new sources of seedling resistance to *Pgt*-TTKSK in the germplasm identified. Studies of the genetic control of resistance and of the allelism of this resistance with known *Pgt*-TTKSK resistance sources are needed to characterize the all-stage resistance present in this germplasm. We have initiated the development and characterization of several populations from the 88 accessions to characterize the genetics of resistance in these lines and develop molecular markers linked to resistance genes effective to *Pgt*-TTKSK.

Table 6.1. Races of *Puccinia graminis* f. sp. *tritici* used to screen United States spring wheat accessions

***Pgt* Race**	**Isolate**	**Virulence/Avirulence Formula**
BCCBC	74JBR-1-111	9g,17,McN/ 5,6,7b,8a,9a,9d,9e,9b,10,11,21,24,30,31,36,38,Tmp
MCCFC	59KS19	5,7b,9g,10,17,McN,Tmp/ 6,8a,9a,9d,9e,9b,11,21,24,31,30,36,38
QFCSC	06ND76C	5,8a,9a,9d,9g,10,17,21,McN/ 6,7b,9e,9b,11,24,31,30,36,38,Tmp
QTHJC	75ND717C	5,6,8a,9b,9d,9g,10,11,17,21,McN/ 7b,9a,9e,24,30,31,36,38,Tmp
RCRSC	77ND82A	5,7b,9a,9b,9d,9g,10,17,21,36,McN/ 6,8a,9e,11,24,30,31,38,Tmp,
RKQQC	99KS76A	5,6,7b,8a,9a,9b,9d,9g,21,36,McN/ 9e,10,11,17,24,30,31,38,Tmp
TPMKC	74MN1409	5,7b,8a,9d,9e,9g,10,11,17,21,36,Tmp,McN/ 6,9a,9b,24,30,31,38
TTTTF	01MN84A-1-2	5,6,7b,8a,9a,9b,9d,9e,9g,10,11,17,21,30,36,McN, Tmp/24,31,38
TTKSK [a]	04KEN156/04	5,6,7b,8a,9a,9b,9d,9e,9g,10,11,17,30,31,38,McN/ 24,36,Tmp
TTKST	06KEN19-V-3	5,6,7b,8a,9a,9b,9d,9e,9g,10,11,17,24,30,31,38,McN/ 36,Tmp

[a] *Sr21* is not included in the formula for races TTKSK or TTKST.

Table 6.2. Seedling infection types and adult plant infection responses and severities of *T. aestivum* accessions to *Puccinia graminis* f. sp. *tritici*

Accession	TPMKC	TTTTF	TTKSK[†]	TTKST	2005 Njoro	2006 Njoro	2007 Njoro	2006 Saint Paul
CI 11649	3	3	3	4	40 MR	30 MS	1 MS	5 MR-MS
CI 11781	4	4	4	4	20 MR	30 S	1 M	5 MR-MS
CI 11782	3-	3	;13	3;	10 MR	1 R	1 MR	5 R
CI 11783	22+	4	;1	3+;	10 MR	10 MS	1 MS	TR
CI 11945	3	32+	0;	0	10 R	1 R	1 MR	10 MR-MS, TS
CI 12040	3	3	3+	3	30 M	5 MR	1 R	5 R
CI 12044	3	42+	X-	3-;	20 MR	2 MR	1 R	T MR
CI 12048	4	3+	0;	0;1+	20 MR	5 R	1 R	T R
CI 12303	3+	32	0;	;3	20 MR	2 R	1 R	5 MR
CI 12324	3+	32	;3	;3-	10 MR	1 R	1 R	T R-MR
CI 12355	3+	4	;13	;3	60 S, 20 MR	1 R	1 R	T R
CI 12433	3+	32	0	;13	5 R	0	1 R	T R
CI 12499	3+	3+	;3	;3-	10 M	1 MR	1 R	T R
CI 12636	4	3+	;3	;3	20 MR	5 MR	1 R	5 MR
CI 12699	2	2-	4	2+3	40 M	5 MR	10 MS	T R
CI 12737	3	3	;3	;23	20 MR	1 R	1 R	5 MR
CI 12780	3	3-	;3	3	40 MR	1 R	1 MS	5 S
CI 12899	;N	2	X-N	;3/3	10 MR	10 MS	1 R-MR	T MR
CI 13100	;2N	3	4	3+	20 MS	10 MR/ 10 S	1 MR	T R-MR
CI 13204	1+	1++	X+	;13	80 S, 10 MR	10 M	1 R-MR	0
CI 13407	2	2+/3+	0;	;1	10 R	1 R	5 M	0
CI 13586	;3N	;1+	X-	3-	20 MS	5 MS	1 R	TR
CI 13652	2++	0;	;	;13-	10 MR	5 M	1 R	0
CI 13773	2	0;	;	;13-	20 MR	10 MS	1 R	T R-MR
CI 14142	;	;1	;	;	20 MR	1 R	1 R	0
CI 14249	;1	3-	;12+	0	20 MR	5 M	10 M	T R
CI 14267	;1	;	2-	2N	20 MR	5 R	10 R-MR	0
CI 14275	;13	1+++LIF	;12	;2	20 MR	5 MR	-	0
CI 14282	;13C	0;	0;	0;	5 MR	0	1 MS	0
CI 14334-1	4;	3+	2+	2++	10 MS	5 R	1 R	T MR-MS
CI 14334-2	4;	4	;2	2	-	5 R	1 R	T R
CI 14388	2	;1++ LIF	3	3+	40 MR	30 MS-S	10 M	0
CI 14396	;1-	3- LIF	;1	;1	20 MR	10 MS	10 M	5 MS

Table 6.2 continued.

Accession	TPMKC	TTTTF	TTKSK[†]	TTKST	2005 Njoro	2006 Njoro	2007 Njoro	2006 Saint Paul
CI 15533	0;	;1+ LIF	0;	0	20 M	5 M	1 R	T MR
CI 15536	;	2++	;1	0;	10 M	40 S	10 MS	T MR
CI 15544	0	3	0;	23-	10 MS	30 MS	1 R	10 MS-S
CI 15555	;11++C	0	;12-	2+3	20 MS	40 S	1 MS	T MR
CI 15557	-	-	;1	;13	5 MS	5 MS	1 R	T MR
CI 15564	2++	32+	;1	2+	20 MS	10 MS	1 R	5 MS
CI 15612	;1-	0;	;	-	40 S, 10 MR	5 MS	1 R	0
CI 15623	0;	0;	0;	;2	20 MS	5 MS	1 R	0
CI 15624	0;	0;	0;	;1	10 MR	5 MS	1 R	0
CI 15658	0;	2++	;	;13	10 R	1 MS	0	0
CI 15679	;12-	3+	3	3-	20 MR	10 MS	1 R	0
CI 15680	2	0	3	3	20 MR	5 R-MR /10 MS	1 R	0
CI 15681	2;	;1	3	3	10 MR	5 R-MR	1 MS	T MR
CI 15682	2;	0;	4	-	20 MS	5 R-MR /5 S	0	0
CI 15685	3	1++	0;	0;1-	5 R	0	0	0
CI 15686	2;	3+	3+	4	10 R	10 MS-S	0	T MR
CI 15711	0;	-	0;1	;1-	20 MR	10 MS	0	5 R-MR
CI 15716	;13C	3+	0;	-	10 MR	30 R/ 10 MS	1 MR	5 MR
CI 15853	-	-	3	3-	5 MR	-	5 R	-
PI 185876	3	3+	23-C	4	30 MR	20 MR/ 40 MS	5 R	10 MR-MS
PI 199813	-	-	4	3	20 MR	10 MS	1 MS	-
PI 234234	-	-	4	4	5 MR	-	70 S	-
PI 234235	3	4	0;	0	5 R	0	30 MSS	5 MR, TS
PI 234236	4	4	0	0	5 R	0	40 MSS	5 MS-S
PI 234237	3 LIF	4	0	0	5 R	0	1 MS	5 MR-MS
PI 234238	-	2++	0;	0	5 R	0	1 MS	5 MS
PI 234239	32;	2++	0;	0;	5 R	0	1 MS	5 MR-MS
PI 238391	32	2++	0;	;13	30 MR	5 M	1 MS	5 MR
PI 254119	3+2	32+	X	3	20 MS	5 MR	1 MR	10 MS
PI 254121	;3N	3+	0	;	10 MS	1 MR	1 R	5 MS
PI 254124	4	3+	0	4	10 MR	1 R	5 MS	10 MR-MS
PI 254126-2	-	-	0	;1	10 MR	1 R	1 MR	5 MS
PI 254137	2+N	22+	;2C	3;	20 MR	1 MR	0	T MS

Table 6.2 continued.

Accession	TPMKC	TTTTF	TTKSK†	TTKST	2005 Njoro	2006 Njoro	2007 Njoro	2006 Saint Paul
PI 254138	3	2+	;3-	-	60 S, 20 MR	5 MS-S	5 MR	60 S
PI 286545	3+	3	4	4	20 MS	5 MR	1 MR	5 MR
PI 286546	2	2	3+	4	20 MS	1 M	1 MR	0
PI 297024	2++	4	;1-	;	10 MR	0	0	0
PI 299414	;1C	;	3-	2++	10 MR	5 MS	5 MS	0
PI 323400	;23	2-3	0	0	5 MR	0	1 MR	0
PI 410954	2	2	2-	2++	20 MS	0	5 R	T MR
PI 480270	;2	3+	;1-	0;	10 M	0	5 MS	0
PI 518648	2	0;	3	3	40 MR	30 S	5 M	0
PI 519501	;1	2- LIF	0	0	10 MR	5 M	1 R	0
PI 519503	3-C	0;1	0	0	10 MS	5 MS	0	0
PI 519553	0	-	0	0	10 R	0	1 MS	0
PI 519623	2N	4	3	31	20 R	20 MS-S	5 M	0
PI 519681	0;	0;	3-	3	10 R	30 MS-S	5 M	T MR/ 20 MS
PI 519711	0;	0;/;2	0	0	10 R	0	0	0
PI 519720	;3-	1-3	0;	0	10 R	0	0	0
PI 519805	2	2-	1	2	10 R	1 MR	5 M	0
PI 519943	0	3+	0	0	10 MR	0	0	0
PI 520033	1+	;	0;	0	10 R	0	1 R	0
PI 520093	0	0	0	0	5 R	0	1 R/5 S	0
PI 520265	2	0;	0	2+	10 MR, 50 S	0	5 MS	0
PI 520373	2	3-	0	3-	5 MS	10 MS-S	1 M	0
LMPG-6	4	2+	3	4	60 MS-S	60 S	70 S	60 S

† The most frequent infection type observed among four replications is listed. Data of all replications are available in Appendix IV.

Chapter VII

Mapping of wheat stem rust resistance gene *Sr13* in hexaploid wheat

Summary

Epidemics of wheat stem rust, caused by *Puccinia graminis* f. sp. *tritici*, in Eastern Africa have been found on varieties that were previously resistant. The susceptibility of current varieties to stem rust has been attributed to the emergence of a virulent race of *P. graminis* f. sp. *tritici*: TTKSK (or Ug99). The majority of wheat varieties worldwide are susceptible to race TTKSK, and only one gene, *Sr13*, is known to confer resistance in durum wheat germplasm. Synthetic hexaploid wheats, created through the merger of a tetraploid wheat genome (AABB) with a diploid *Aegilops tauschii* genome (DD), have been used in breeding to introgress traits from both *A. tauschii* and tetraploids to hexaploid bread wheat. We describe that resistance to race TTKSK in a synthetic hexaploid wheat derivative, TA4152-37, is conferred by *Sr13*. We screened 120 $F_{2:3}$ progeny of the cross between TA4152-37 and susceptible Chinese Spring for resistance to races TTKSK and TTTTF. To identify molecular markers linked to *Sr13*, F_2 DNAs were screened with DArT and SSR markers. Previous studies mapping *Sr13* in tetraploid wheat failed to identify diagnostic markers or markers closely linked and flanking the *Sr13* locus. We report the mapping of *Sr13* to the distal region of chromosome arm 6AL and the detection of flanking DArT markers wPt-8773 and wPt-5696, 2.9 cM and 2.4 cM respectively away from *Sr13*. The sequences available for the flanking DArT markers could be used to develop SNP markers for use in marker-assisted selection.

Introduction

Wheat stem rust, caused by the basidiomycete fungus *Puccinia graminis* f. sp. *tritici*, is historically one of the most devastating diseases of wheat. In the United States, stem rust yield losses reached 56% and 43% in North Dakota in 1935 and 1954, respectively (Leonard, 2001). Breeding for resistant varieties of wheat in combination with the eradication of the alternate host of stem rust, *Berberis vulgaris*, in the United States effectively controlled stem rust for the past several decades. The deployment of resistant varieties worldwide has similarly reduced the frequency and severity of stem rust epidemics.

In 1998, researchers observed stem rust infection on previously resistant varieties of wheat in Uganda (Pretorius et al., 2000). Isolates of *P. graminis* f. sp. *tritici* from Uganda and Kenya were described as race TTKSK (Ug99; *Pgt*-TTKSK) according to the North American stem rust differential set (Jin et al., 2008). Screening of cultivars indicated that race TTKSK was virulent on the majority of currently grown cultivars in the United States, Canada, and Asia (Jin and Singh, 2006; Fetch, 2007; Singh et al., 2008). These results indicated that if *Pgt*-TTKSK were to spread throughout the world, it could become a significant limitation to the global wheat supply. The observation of epidemics of stem rust in Kenya in 2004 by Nobel Peace Prize laureate Norman Borlaug initiated a global effort to breed resistant varieties of wheat and barley to *Pgt*-TTKSK (Singh et al., 2006).

Unfortunately, *Pgt*-TTKSK is spreading throughout eastern and southern Africa and the Middle East, infecting wheat in Yemen in 2006, in Iran in 2007, and South Africa in 2009 (Singh et al., 2008; Nazari et al., 2009; Pretorius et al., 2010). Variants of *Pgt*-TTKSK have been detected with additional virulence to resistance genes *Sr24* and *Sr36* and classified as races TTKST and TTTSK, respectively (Jin et al., 2008; Jin et al., 2009). These variants are significant because much of the resistance to *Pgt*-TTKSK in hard and soft winter wheat cultivars in the United States is conferred by *Sr24* and *Sr36*, respectively. Race TTKST (*Sr24*-virulent) has been detected at a high frequency in the last few years in Kenya. This is likely due to the deployment of varieties with *Sr24* used to provide resistance to race TTKSK (*Sr24*-avirulent). This 'boom and bust' cycle where a resistant variety is deployed followed by selection in the pathogen population resulting in disease epidemics is common for the cereal rusts. In order to prevent further deployment and breakdown of stem rust resistance, it will be important to combine multiple sources of resistance in cultivars so that the pathogen cannot adapt as rapidly.

Approximately 50 wheat stem rust resistance genes are known and markers have been developed linked to several of these genes (McIntosh et al., 2008; a table cataloguing markers linked to stem rust resistance genes is available at http://rustopedia.get-traction.com/traction). Many of these resistance genes have been introgressed into wheat from wild relatives. One method to introgress resistance genes from wild relatives to hexaploid wheat is the use of synthetic hexaploids. Synthetic hexaploid wheats are the product of the merger between a tetraploid AABB genome wheat and a diploid DD genome (*Aegilops tauschii*). We found that a synthetic hexaploid

derivative, TA4152-37, exhibited resistance to race TTKSK in greenhouse assays. Our objective was to determine the genetics of resistance in TA4152-37 and to map this resistance with DArT and SSR markers in order develop markers linked to this resistance.

Materials and methods

Plant material

Synthetic hexaploid wheat TA 4152-37, with resistance to *Pgt*-TTKSK, was crossed with Chinese Spring (CSA). TA 4152-37 was developed by CIMMYT (pedigree: 68.11/RGB-U//WARD/3/FGO/4/RABI/5/*A. tauschii* (878), Chu et al., 2006). 120 $F_{2:3}$ families were derived. In order to test for allelism between resistance in TA 4152-37 and *Sr13*, TA 4152-37 was crossed to Combination VII and Khapstein/9*LMPG (hexaploid genetic stocks for *Sr13*). 115 and 216 F_2 progeny were derived for the respective populations.

Phenotypic analyses of stem rust

Isolates 04KEN156/04 and 01MN84A-1-2 (races TTKSK and TTTTF, respectively) of *Pgt* were used for inoculating the TA4152-37/CSA population in two separate treatments. 04KEN156/04 was used to inoculate the F_2 progeny of TA4152-37/Combination VII and TA4152-37//Khapstein/9*LMPG. Isolate 04KEN156/04 corresponds to Ug99 as described previously (Jin et al., 2007; Jin et al., 2008). The avirulence/virulence formulae for the isolates are displayed in Table 7.1. *Pgt*-TTKSK is known to be avirulent to *Sr13* (Jin and Singh, 2006). Urediniospores in gelatin capsules stored at -80°C were heat-shocked at 45°C for 15 min, and placed in a rehydration chamber for 2 to 4 h maintained at 80% relative humidity by a KOH solution (Rowell, 1984). Procedures for inoculation, incubation and disease assessment were performed as

described previously (Jin et al. 2007). Infection types (ITs) were classified as in Stakman et al. (1962). ITs '0' to '2' were considered incompatible interactions between the pathogen and host, indicating host resistance, whereas ITs '3' and '4' were considered compatible interactions between the pathogen and host, indicating host susceptibility. A total of 15-20 plants from each $F_{2:3}$ family were screened with each race. The $F_{2:3}$ families were classified as homozygous resistant, homozygous susceptible, or heterogeneous in reaction to races TTKSK and TTTTF.

Molecular marker analyses

Tissue was harvested from the 120 TA 4152-37/CSA F_2 plants corresponding to the $F_{2:3}$ families. DNA was extracted for each F_2 plant using a CTAB method following Riede and Anderson (1996) with modifications by Liu et al. (2006) and further modifications including the use of a bead grinder (FastPrep®-24, MP Biomedicals, Inc.) to pulverize plant tissue. A total of 92 F_2 DNAs and DNA of the parents were genotyped with diversity arrays technology (DArT) markers according to Akbari et al. (2006). Four SSR markers previously identified as linked to *Sr13* were also genoypted for the same 92 F_2 extracts, two additional F_2 extracts, and the parents (Simons et al., 2010). SSR genotyping involved the amplification of the markers (barc104, gwm169, gwm427, and wmc580) in 10 µL PCR reactions with 1 X PCR buffer (New England Biolabs, Inc. Beverley, MA), 0.125 mM dNTPs, 0.4 pmol forward primer, 0.3 pmol reverse primer, 3.0 pmol of M13 primer (labeled with one of the following fluorescent dyes: 6-FAM, NEC, PET, and VIC), 0.05 units/µL Taq DNA polymerase (New England Biolabs), and 45 ng

of genomic DNA. Marker barc104 is from Song et al. (2005), the gwm markers are from Roder et al. (1998), and wmc580 is from Somers et al. (2004). All PCR reactions were run on GeneAmp PCR system 9700 thermocyclers (Applied Biosystems, Foster City, CA) and denatured at 94ºC for 10 minutes, cycled through 94ºC for 1 minute, 50ºC for 1 minute, and 72ºC for 1 minute 40 times, kept at 72ºC for 5 minutes, and at 4ºC permanently. Four PCR reactions with different fluorescent dyes were multiplexed and 3 µL were combined with 0.14 µL size standard (GeneScan-500 LIZ®, Applied Biosystems) and 6.86 µL formamide (Hi-Di™, Applied Biosystems). The mixtures were denatured at 94ºC for 5 minutes and then placed on ice. Amplified fragments were analyzed using an ABI 3130xl Genetic Analyzer (Applied Biosystems) and GeneMapper software v3.7 (Applied Biosystems).

Segregation and linkage

Chi-square tests were performed to test for deviation of observed segregation ratios compared to expected segregation ratios. An initial genetic map was constructed for the stem rust resistance locus and SSR markers using Joinmap v4.0 (Stam, 1993; van Ooijen, 2006). Genetic distances were calculated using Kosambi's distance estimate and assignment of markers to linkage groups was completed using a logarithm of odds value of 5.0. In order to map the dominant DArT markers, we followed the technique used by Jing et al. (2009) where maternal DArT markers (scored as 'a or 'c') were initially mapped separately with the codominant markers, then the paternal markers (scored as 'b' or 'd'). Using the 'combine maps' function in Joinmap, the two maps were then merged

using the SSR markers and stem rust resistance locus as bridge markers.

Results

Stem rust phenotypic analyses

For the mapping population, ITs of parents were '2,2+' for TA 4152-37 and '4' for Chinese Spring in reaction to both isolates. In reaction to *Pgt*-TTKSK, many of the $F_{2:3}$ progeny displayed the infection types '2+3' or '3' making discrimination between resistant and segregating families difficult. In contrast, few '2+3' infection types were observed in reaction to race TTTTF. The difficulty in discriminating between resistance and susceptibility to race TTKSK was reflected in the segregation of resistance. For race TTTTF, segregation of $F_{2:3}$ families did not deviate significantly from 1:2:1 for resistant:segregating:susceptible (22:51:36, X^2=4.05, *df*=2, *P*=0.132). However, segregation of resistance to race TTKSK did deviate significantly from 1:2:1 (14:49:54, X^2=30.4, *df*=2, *P*=2.46E-7) with a bias towards an increased number of susceptible families and a decreased number of resistant families. Resistance to race TTKSK did not segregate independently from race TTTTF (X^2=71.8, *df*=8, *P*=2.13E-12). The evidence suggest that the discrepancy between segregation ratios between races TTTTF and TTKSK is due to the difficulty in discriminating between resistance and susceptibility to race TTKSK and not due to independent genes conferring resistance to races TTKSK and TTTTF. Since the reaction of the population to race TTTTF was clear and did not deviate significantly from 1:2:1, the reaction to race TTTTF was used for mapping a single dominant gene in TA4152-37.

Preliminary linkage analyses of resistance to race TTTTF with DArT markers

indicated that the resistance gene was located on chromosome arm 6AL. Gene *Sr13* was mapped to chromosome arm 6AL by McIntosh (1972) using monosomic analyses. In order to determine if resistance in TA4152-37 is conferred by *Sr13*, we crossed TA4152-37 with monogenic lines with *Sr13*, Combination VII and Khapstein/9*LMPG. All of the 115 TA4152-37/Combination VII and 216 TA4152-37//Khapstein/9*LMPG F_2 plants screened with TTKSK displayed ITs '2' to '2+3'. Since the parents also displayed ITs '2,2+' to '2+3' to race TTKSK, resistance in TA4152-37 to race TTKSK is likely conferred by *Sr13*. Since TA4152-37 is a synthetic derivative, and *Sr13* is known to exist in some tetraploid wheats, it is possible that TA4152-37 obtained *Sr13* from the tetraploid in its pedigree: RABI. Since the mapped location of race TTTTF resistance is consistent with the previously mapped location of *Sr13* in tetraploid wheat (see results, Simons et al., 2010), there is no evidence to suggest that race TTTTF resistance is independent of *Sr13*. The race TTTTF resistance locus will now be referred to as *Sr13*.

Genetic segregation, linkage, and mapping

A total of 388 polymorphic DArT markers were identified. When constructing a linkage map with the DArT markers and *Sr13*, *Sr13* was linked to ten DArT markers (wPt-1661, wPt-1695, wPt-2216, wPt-3247, wPt-5696, wPt-7204, wPt-8124, wPt-8764, wPt-8773, and wPt-9976). Markers wPt-8124 and wPt-1661 were previously mapped to 6AL (Akbari et al., 2006). Segregation of DArT and SSR markers are displayed in Table 7.2. Three of the four SSR markers and the seven DArT markers that hybridized with the paternal (TA4152-37) allele displayed significant segregation distortion. *Sr13* exhibited

segregation distortion of marginal significance when tested among the 94 families that were selected for molecular marker analyses (*Sr13*, synonymous with race TTTTF resistance, did not exhibit segregation distortion when tested at a larger sample size as described earlier). In all cases, the segregation distortion was caused by an unexpectedly high amount of paternal alleles (TA4152-37, *Sr13*).

A map was constructed integrating both the SSR and DArT markers linked to *Sr13* (Figure 7.1). Genotypic and phenotypic data used for constructing the linkage map are available in Appendix V. The order and distances between *Sr13* and the SSR markers are consistent with previously constructed maps for *Sr13* in tetraploid wheat (Figure 7.1, Simons et al., 2010). Seven of the ten DArT markers mapped in between *Sr13* and the SSR markers flanking *Sr13*. The two closest flanking DArT markers were wPt-8773 and wPt-5696 (2.9 cM proximal and 2.4 cM distal to *Sr13*, respectively).

Discussion

Three major findings of this research are (1) the identification of *Sr13* as mediating the stem rust resistance to races TTKSK and TTTTF in the synthetic hexaploid wheat derivative TA4152-37, (2) the validation that the location of *Sr13* in hexaploid wheat is consistent with the location in tetraploid wheat, based upon mapping molecular markers, and (3) the identification of DArT markers closely linked and flanking *Sr13*.

Synthetic hexaploid derivative TA4152-37 was identified as resistant to stem rust race TTKSK (Ug99) in seedling assays. We demonstrated that this resistance is mediated by *Sr13* through allelism tests with hexaploid genetic stocks carrying *Sr13*, and by mapping the resistance to the same location where *Sr13* was mapped in tetraploid wheat (Simons et al., 2010). Since TA4152-37 is a synthetic derivative, and *Sr13* is known to be located in several tetraploid wheats, TA4152-37 likely inherited *Sr13* from the tetraploid parent of the synthetic: RABI.

Simons et al. (2010) mapped *Sr13* on 6AL in between SSR markers barc104 and gwm427/wmc580. We validated that *Sr13* maps in between these SSR markers in hexaploid wheat. Though Simons et al. (2010) developed several SNP and STS markers in the *Sr13* region, diagnostic markers were not identified. We identified ten DArT markers linked to *Sr13* in this study, seven of which were mapped in between *Sr13* and the nearest flanking SSR markers. The sequences available for these markers could be used to develop SNP markers flanking *Sr13*. Further studies are needed to develop these markers, and determine whether or not they are diagnostic for *Sr13* in diverse germplasm.

Developing markers linked to *Sr13* will facilitate the breeding of resistant varieties of wheat to stem rust with multiple resistance genes.

Table 7.1. Avirulence/virulence formulae of isolates of *Puccinia graminis* f. sp. *tritici*

Isolate	Race	Avirulence	Virulence
01MN84A-1-2	TTTTF	*13 24 31*	*5 6 7b 8a 9a 9b 9d 9e 9g 10 11 17 21 30 36 38 McN*
04KEN156/04	TTKSK [a]	*13 24 36 Tmp*	*5 6 7b 8a 9a 9b 9d 9e 9g 10 11 17 30 31 38 McN*

[a] *Sr21* is not included in the formula for *Pgt*-TTKSK.

Table 7.2. Segregation of *Sr13* and markers linked to *Sr13* among 94 F_2 individuals or $F_{2:3}$ families used for mapping

Marker/Gene	a[a]	h	b	c	d	Total	X^{2} [b]	*P* value
Sr13	21	38	32	-	-	91	5.13	0.08
barc104	17	40	25	-	-	82	1.61	0.45
gwm427	20	28	29	-	-	77	7.83	0.02
wmc580	20	22	23	-	-	65	7.06	0.03
gwm169	13	29	27	-	-	69	7.43	0.02
wPt-1661	21	-	-	65	-	86	0.02	0.90
wPt-1695	24	-	-	61	-	85	0.47	0.49
wPt-8124	24	-	-	57	-	81	0.93	0.34
wPt-8764	-	-	37	-	45	82	17.71	2.58E-05
wPt-8773	-	-	37	-	48	85	15.56	7.97E-05
wPt-5696	-	-	34	-	52	86	9.69	1.85E-03
wPt-2216	-	-	33	-	56	89	6.93	8.50E-03
wPt-3247	-	-	31	-	50	81	7.61	5.81E-03
wPt-7204	-	-	32	-	57	89	5.70	0.02
wPt-9976	-	-	29	-	51	80	5.40	0.02

[a] 'a' refers to homozygous for the Chinese Spring allele, 'h' refers to heterozygous, 'b' refers to homozygous for the TA4152-37 allele, 'c' refers to either heterozygous or homozygous TA4152-37, and 'd' refers to heterozygous or homozygous Chinese Spring.

[b] X^2 values calculated for testing 1:2:1 segregation for codominant markers (2 df) or 1:3 segregation for dominant markers (1 df)

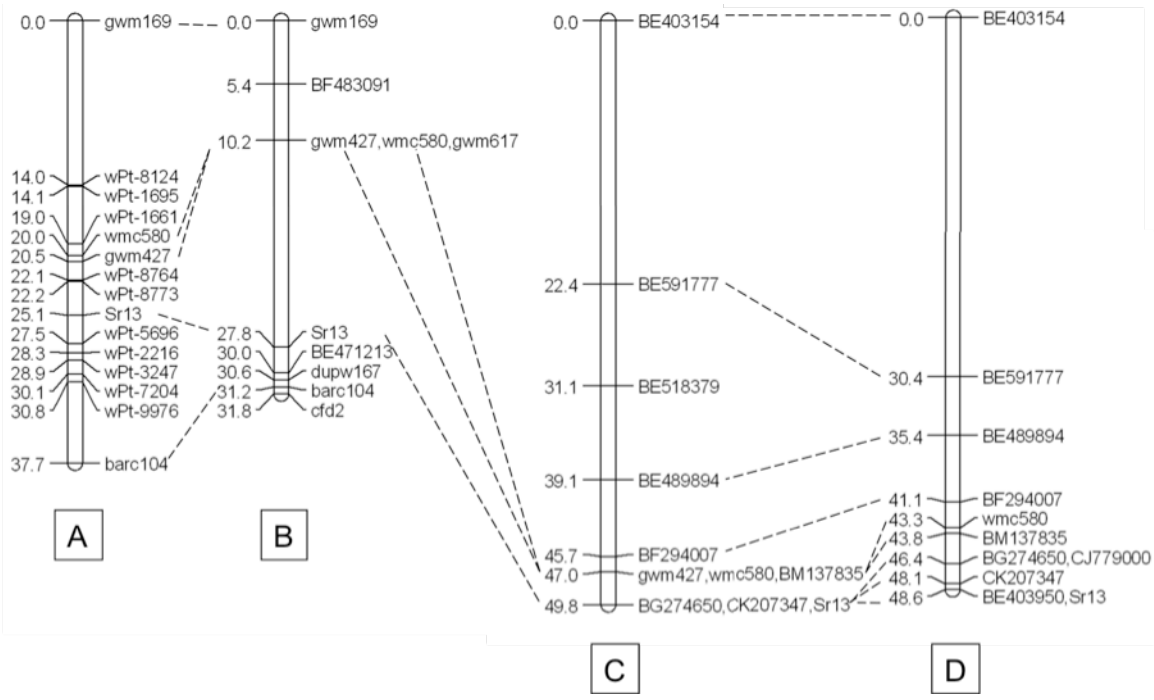

Figure 7.1. *Sr13*, DArT, and SSR marker linkage map of chromosome 6AL from the cross TA 4152-37/CSA (A), and maps of *Sr13* linkage groups in tetraploid wheat from Simons et al. (2010): UC1113/Kofa (B), Mindum/Sceptre (C), and Mindum/Medora (D)

Chapter VIII

Genetics and mapping of resistance to *Puccinia graminis* f. sp. *tritici* race TTKSK in Gabo 56 wheat

Summary

Race TTKSK (Ug99) of *Puccinia graminis* f. sp. *tritici*, the causal fungus of stem rust, threatens global wheat production because of its virulence to many stem rust resistance genes in current wheat cultivars. Identification of resistance to TTKSK and development of linked molecular markers will facilitate breeding resistant cultivars. We describe the genetics and mapping of resistance in hexaploid wheat cultivar Gabo 56. Gabo 56 is a Rockefeller Foundation cultivar released in 1956 that displays resistance to Ug99 in Kenya (30-40% R-MR infection). The $F_{2:3}$ progeny of a cross between Gabo 56 and susceptible Chinese Spring were evaluated with race TTKSK. Resistance in Gabo 56 was inherited as a single dominant gene we refer to as *SrGabo56*. This resistance locus was mapped to chromosome 2BL using DArT and microsatellite markers, the closest microsatellite marker being gwm47. Alleles of the *Sr9* locus mapped to similar chromosome locations in previous studies. Further studies are needed to determine the genetic relationship between *SrGabo56* and *Sr9*. Flanking DArT markers tightly linked to *SrGabo56* were identified that could be used to develop markers amenable to marker assisted selection. The identification and characterization of *SrGabo56* as a race TTKSK resistance gene in hard red spring wheat germplasm provides breeders with a rare utilizable source of resistance to Ug99.

Introduction

Puccinia graminis f. sp. *tritici* (*Pgt*), the causal agent of wheat stem rust, has been one of the most significant wheat diseases historically. In North America, epidemics of wheat stem rust were responsible for yield losses greater than 40% across North Dakota and Minnesota during years conducive for disease development in the 1930's and 1950's (Leonard, 2001). Major efforts to control this disease including breeding resistant varieties and elimination of the alternate host, *Berberis vulgaris*, from wheat growing regions have been successful in controlling stem rust in North America. Similarly, the deployment of resistant varieties of wheat worldwide, including many varieties with stem rust resistance gene *Sr31*, has resulted in the successful control of stem rust for the past several decades.

In 1999, a race of *Pgt* was reported from Uganda that possessed unique virulence to *Sr31* in addition to virulence to many stem rust resistance genes currently used in agriculture (Pretorius et al., 2000). This race, known as Ug99, was formally described as race TTKSK according to the North American stem rust nomenclature (*Pgt*-TTKSK; Jin et al., 2008). The unique virulence combination in *Pgt*-TTKSK was hypothesized to be a dangerous threat to the global wheat crop and screening studies subsequently demonstrated that the majority of cultivars grown in the United States and Canada in addition to nearly all of the cultivars grown in Asia are susceptible (Fetch, 2007; Jin and Singh, 2006; Singh et al., 2008). In the hard red spring market class of United States

wheat, historically the most vulnerable to epidemics of stem rust, 84% of breeding lines and current cultivars are susceptible to *Pgt*-TTKSK (Jin and Singh, 2006).

Pgt-TTKSK was hypothesized to spread out of eastern Africa into Asia along predominant wind trajectories (Singh et al., 2006). *Pgt*-TTKSK was found in Yemen in 2006 and in Iran in 2007 (Nazari et al., 2009). Variants of *Pgt*-TTKSK have been identified in Kenya with additional virulence to resistance genes *Sr24* and *Sr36* (Jin et al., 2008; Jin et al., 2009). Virulence to these genes is significant since *Sr24* and *Sr36* are present in a large proportion of the lines resistant to *Pgt*-TTKSK (Jin and Singh, 2006). Also, *Pgt*-TTKSK variants that are avirulent to *Sr21* relative to the original *Pgt*-TTKSK isolates have been identified in South Africa (Pretorius et al., 2010). The spread of *Pgt*-TTKSK and variants throughout Africa and the Middle East demonstrate the immediacy of identifying and utilizing resistant wheat varieties. The identification of variants of *Pgt*-TTKSK with additional virulence indicate that combinations of resistance genes will need to be deployed in cultivars in order to provide effective and durable resistance to *Pgt*-TTKSK.

Several resistance genes have been identified that are effective to *Pgt*-TTKSK (Jin et al., 2007). However, the majority of these genes are less likely to be used because of (1) their linkage to undesireable traits, (2) their ineffectiveness to other races of *Pgt*, and (3) their relatively low effectiveness to *Pgt*-TTKSK. For example, only eight of the currently named resistance genes provide resistance to *Pgt*-TTKSK and are derived from the primary gene pool of wheat (Jin et al., 2007). Of these eight genes, only two are effective to all described races of *Pgt* (*Sr22* and *Sr33*; Huerta-Espino, 1992). *Sr33*

provides only moderate resistance to *Pgt*-TTKSK at the adult plant stage in the field (Jin et al., 2007). Additional sources of resistance to *Pgt*-TTKSK are needed.

Gabo 56 (CI 14035), is a Rockefeller Foundation wheat cultivar released in 1956 that displayed both seedling and adult plant resistance to *Pgt*-TTKSK in preliminary screening (30-40% severity and R-MR infection response in Kenya in 2007 through 2009). Our objectives were to describe the genetics of resistance to *Pgt*-TTKSK in Gabo 56 and to map this resistance.

Materials and methods

Plant material and stem rust phenotyping

Gabo 56 (CI 14035; pedigree Timstein/Kenya 58//Gabo) seed was obtained from the United States Department of Agriculture National Small Grains Collection (Aberdeen, ID). Gabo 56 was crossed with susceptible Chinese Spring (CSA) and 104 $F_{2:3}$ families were developed. Isolate 04KEN156/04 of *Pgt* was used for inoculating the Gabo 56/CSA population. Isolate 04KEN156/04 is race TTKSK (Ug99; Jin et al., 2007; Jin et al., 2008). Urediniospores in gelatin capsules stored at -80°C were heat-shocked at 45°C for 15 min, placed in a rehydration chamber for 2 to 4 h maintained at 80% relative humidity by a KOH solution (Rowell, 1984), and suspended in a light mineral oil (Soltrol 70, ConocoPhillips Inc., Houston, TX). Procedures in inoculation, incubation and disease assessment were followed as described previously (Jin et al. 2007). Infection types (ITs) were classified as in Stakman et al. (1962). Infection types '0' to '2' were considered low infection types indicating host resistance, whereas ITs '3' to '4' were considered high infection types indicating host susceptibility. The population was assayed for reaction to stem rust in two replications. In each replication, 15-20 plants from each $F_{2:3}$ family were screened with *Pgt*-TTKSK. $F_{2:3}$ families were classified as homozygous resistant, homozygous susceptible, or heterogeneous in reaction to *Pgt*-TTKSK. Segregation of resistance was evaluated for deviation from expected ratios using a chi-square goodness-of-fit test.

In order to test if seedling resistance to *Pgt*-TTKSK corresponded to adult plant resistance, we evaluated the adult plant infection response of 15 selected $F_{2:3}$ families. Families were selected for homozygosity of reaction to *Pgt*-TTKSK at the seedling stage (either resistant or susceptible). For each family evaluated, 4 plants were evaluated with *Pgt*-TTKSK. Plants were inoculated with *Pgt*-TTKSK at the heading growth stage (Feekes 10.1 to 10.5; Large, 1954). Procedures in inoculation and incubation were followed corresponding to seedling assays. Infection response was recorded 21 days after inoculation. Plants were classified as either resistant (R), moderately resistant (MR), moderately susceptible (MS), or susceptible (S) based upon size of pustules and amount of necrosis and chlorosis according to Roelfs et al. (1992). If a plant displayed multiple infection responses, all were recorded. When families were observed to be heterogeneous for infection response, the most common infection response was recorded, followed by a '/', and followed by the least common infection response.

Molecular marker analyses

Tissue was harvested from the 104 Gabo 56/Chinese Spring F_2 parents of the corresponding $F_{2:3}$ families. DNA was extracted for each F_2 plant using a CTAB method following Riede and Anderson (1996) with modifications by Liu et al. (2006) and further modifications including the use of a bead grinder (FastPrep®-24, MP Biomedicals, Inc.) to pulverize plant tissue. 80 F_2 DNAs and DNA of the parents were genotyped with diversity arrays technology (DArT) markers according to Akbari et al. (2006). Initial mapping of resistance in Gabo 56 with DArT markers indicated linkage of a resistance

gene with DArT markers on chromosome 2BL. Therefore, gwm, barc, and wmc microsatellite markers previously mapped to chromosome 2BL were tested for polymorphism among Chinese Spring and Gabo 56 (gwm markers from Roder et al., 1998; wmc markers from Somers et al., 2004; and barc markers from Song et al., 2005). Resistant and susceptible bulk DNAs of ten plants each were used to select, from the polymorphic markers, microsatellites linked to resistance (Michelmore et al., 1991). The population was then genotyped for the identified microsatellite markers. Microsatellite genotyping involved the amplification of the markers in 10 µL PCR reactions with 1 X PCR buffer (New England Biolabs, Inc. Beverley, MA), 0.125 mM dNTPs, 0.4 pmol forward primer, 0.3 pmol reverse primer, 3.0 pmol of M13 primer (labeled with one of the following fluorescent dyes: 6-FAM, NEC, PET, and VIC), 0.05 units/µL Taq DNA polymerase (New England Biolabs), and 45 ng of genomic DNA. All PCR reactions were run on GeneAmp PCR system 9700 thermocyclers (Applied Biosystems, Foster City, CA) and denatured at 94ºC for 10 minutes, cycled through 94ºC for 1 minute, 50ºC for 1 minute, and 72ºC for 1 minute 40 times, kept at 72ºC for 5 minutes, and at 4ºC permanently. Four PCR reactions with different fluorescent dyes were multiplexed and 3 µL were combined with 0.14 µL size standard (GeneScan-500 LIZ®, Applied Biosystems) and 6.86 µL formamide (Hi-Di™, Applied Biosystems). The mixtures were denatured at 94ºC for 5 minutes and then placed on ice. Amplified fragments were analyzed using an ABI 3130xl Genetic Analyzer (Applied Biosystems) and GeneMapper software v3.7 (Applied Biosystems).

Segregation and genetic linkage

Chi-square tests were performed to test for deviation of observed segregation ratios compared to expected segregation ratios for microsatellite and DArT markers. In order to contruct a linkage map, Joinmap v4.0 (Stam, 1993; van Ooijen, 2006) was used. Genetic distances were calculated using Kosambi's distance estimate (Kosambi, 1944). DArT markers were divided into maternal and paternal classes (maternal markers were scored 'a' or 'c' whereas paternal markers were scored as 'b' or 'd'). A logarithm of odds value of 5.0 was used to identify maternal and paternal DArT markers linked to stem rust resistance. In order to map the dominant markers, we followed the technique used by Jing et al. (2009) where maternal DArT markers were initially mapped separately with the codominant markers, then the paternal markers. Using the 'combine maps' function in Joinmap, the two maps were then merged using the codominant markers and stem rust resistance as bridge markers.

Results

Stem rust phenotypic analyses

Gabo 56 displayed a '2' to '2+' seedling infection type to *Pgt*-TTKSK in contrast to the '4' infection type observed for Chinese Spring. In the $F_{2:3}$ progeny, resistant plants displayed '2' to '2+' infection types and susceptible plants displayed '3' to '4' infection types. In segregating families, sometimes '2+3' infection types were observed (possibly indicative of heterozygous individuals). Segregation of resistance did not deviate significantly from the expected 1:2:1 ratio (resistant:segregating:susceptible) for segregation of a single dominant gene (Table 8.1). We tentatively designate this gene as *SrGabo56*.

The adult plant infection responses of the 15 selected $F_{2:3}$ families are displayed in Table 8.2. Presence or absence of *SrGabo56* was determined based upon the seedling infection type assay. The families that displayed seedling resistance to *Pgt*-TTKSK ('+' for *SrGabo56*) were also resistant at the adult plant stage (Table 8.2).

Genetic segregation, linkage, and mapping

Hybridization of F_2 DNAs to the DArT wheat array indicated the presence of 293 polymorphic DArT markers. Five markers were linked to *SrGabo56* (logarithm of odds value of 5.0; wPt-1140, wPt-3109, wPt-3132, wPt-4199, and wPt-8460). Markers wPt-3132 and wPt-8460 were previously mapped to chromosome arm 2BL (Akbari et al., 2006). Seven microsatellite markers were identified that (1) were polymorphic among

Chinese Spring and Gabo56 and (2) segregated among resistant and susceptible bulks: barc101, gwm47, gwm120, gwm319, gwm388, wmc175, and wmc332. None of the molecular markers deviated from expected segregation ratios (Table 8.1). The marker data for each $F_{2:3}$ individual are available in Appendix VI.

Linkage analyses identified that gwm47 was the microsatellite marker most tightly linked with *SrGabo56* at a distance of 2.8 cM (Figure 8.1C). gwm47 was also linked to *Sr9a* and *SrWeb* in previous studies (Figure 8.1D, 8.1E; Tsilo et al., 2007; Hiebert et al., 2010). Both gwm47 and wmc175 are dominant markers in this population, and linked in repulsion with *SrGabo56* (Table 8.1). The closest DArT markers flanking *SrGabo56* were wPt-3132 1.9 cM proximal to *SrGabo56* and wPt-8460 1.5 cM distal (Figure 8.1C). These markers also flanked the *Yr7*/*Sr9g* locus in a previous study (Figure 8.1B; Akbari et al., 2006).

Discussion

We identified a single dominant gene that confers the resistance in Gabo 56 to race TTKSK of *Pgt*: *SrGabo56*. The resistance conferred by *SrGabo56* was effective at both seedling and adult plant stages. This gene mapped to chromosome arm 2BL. Stem rust resistance genes have previously been mapped to this chromosome arm including *Sr9*, *Sr16,* and *Sr28* (McIntosh et al., 1995). The linkage of *SrGabo56* with gwm47, wPt-3132, and wPt-8460 indicate that *SrGabo56* maps to a similar location as *Sr9a*, *Sr9g*, and *SrWeb* (Figure 8.1; Akbari et al., 2006; Tsilo et al., 2007, Hiebert et al., 2010). Since none of the previously described alleles of *Sr9* displayed resistance to *Pgt*-TTKSK (Jin et al., 2007), if *SrGabo56* is an allele of *Sr9*, it is a new allele. We are currently examining the segregation of resistance to multiple isolates of *Pgt* in a cross between Gabo 56 and Vernstein (*Sr9e*) to determine the allelic relationship between *SrGabo56* and *Sr9e*. *SrWeb* was recently described as a stem rust resistance gene in the accession Webster that confers resistance to *Pgt*-TTKSK (Hiebert et al., 2010). Since *SrWeb* and *SrGabo56* map to a similar location and lines with both genes confer similar seedling and adult plant responses to *Pgt*-TTKSK, it is possible that *SrWeb* and *SrGabo56* are the same gene. Studies are in progress to determine the allelic relationship between *SrWeb* and *SrGabo56*.

Seedling screening of Gabo 56 with diverse races of *Pgt* indicated that resistance in Gabo 56 is race-specific with resistance to North American *Pgt* races QCCSM, MCCFC, QFCSC, TPMKC, RCRSC, SCCSC, and RKQQC, and susceptibility to races

QTHJC and TTTTF (data not shown). It is not possible to determine if the resistance exhibited by Gabo 56 to the diverse races is mediated by *SrGabo56* from the available data. Screening our population with various races could determine whether or not Gabo 56 possesses stem rust resistance genes in addition to *SrGabo56*. We are in the process of backcrossing *SrGabo56* into the stem rust susceptible line LMPG-6. Screening an *SrGabo56* monogenic line with diverse races could elucidate the race-specificity of *SrGabo56*.

The marker order of microsatellite and DArT markers on our 2BL linkage map is consistent with previous studies with the exception of wmc175. This marker mapped to different locations in each population analyzed relative to gwm47 and gwm120 (Figure 1C, 1D, 1E). One reason for the inconsistency of the location of wmc175 relative to the order of other markers may be caused by the dominant inheritance of this marker, which may result in less accurate data compared to codominant inheritance.

The construction of a map of *Pgt*-TTKSK resistance in Gabo 56 is the first step towards identifying markers for use in marker-assisted selection. Though gwm47 is a dominant marker that is tightly linked with both *SrWeb* and *SrGabo56*, it is linked in coupling with *SrWeb* and in repulsion with *SrGabo56*. Therefore, gwm47 is not ideal for use in marker-assisted selection of *SrGabo56*. The sequences of the DArT markers identified that flank *SrGabo56* could be used to design PCR-based markers tightly linked to *SrGabo56*.

SrGabo56 could be used in breeding to provide resistance to race TTKSK. Since Gabo 56 is a hard red spring wheat cultivar, introgression of *SrGabo56* into adapted

germplasm is likely to be obtained without linkage drag. The race-specificity of Gabo 56 and the detection of variants of *Pgt*-TTKSK with additional virulence suggest that the deployment of *SrGabo56* alone will not result in durable resistance to *Pgt*-TTKSK. The development of utilizable markers linked to *SrGabo56* could facilitate the pyramiding of this gene with other stem rust resistance genes effective to *Pgt*-TTKSK. The identification and characterization of additional sources of resistance to *Pgt*-TTKSK are needed to provide breeders with the tools to obtain effective and durable resistance to *Pgt*-TTKSK and other races of stem rust.

Table 8.1. Segregation of *Pgt*-TTKSK resistance and linked markers among F_2 individuals or $F_{2:3}$ families used for mapping

Marker/Gene	a[a]	h	b	c	d	Total	X^{2} [b]	*P* value
gwm319	23	35	14	1	6	79	2.72	0.26
gwm388	21	40	10	8	-	79	4.9	0.09
wPt-4199	19	-	-	41	-	60	1.42	0.23
wPt-3109	-	-	17	-	37	54	1.21	0.27
wmc175	22	-	-	58	-	80	0.27	0.61
wPt-1140	-	-	14	-	45	59	0.05	0.82
barc101	18	39	20	1	-	78	0.13	0.94
gwm120	19	40	21	-	-	80	0.1	0.95
gwm47	23	-	-	55	-	78	0.84	0.36
wPt-3132	-	-	12	-	43	55	0.3	0.59
TTKSK	35	48	21	-	-	104	4.38	0.11
wPt-8460	19	-	-	40	-	59	1.63	0.2
wmc332	20	43	16	-	-	79	1.03	0.6

[a] 'a' refers to homozygous for the Gabo 56 allele, 'h' refers to heterozygous, 'b' refers to homozygous for the Chinese Spring allele, 'c' refers to either heterozygous or homozygous Chinese Spring, and 'd' refers to heterozygous or homozygous Gabo 56.

[b] X^2 values calculated for testing 1:2:1 segregation for codominant markers (2 df) or 3:1 segregation for dominant markers (1 df). Occasional inidividuals classified as 'c' or 'd' were not included in calculaiton of X^2 values for codominant markers.

Table 8.2. Adult plant infection responses (IR) of selected homozygous resistant or susceptible $F_{2:3}$ families

$F_{2:3}$ Family	***SrGabo56***	**IR** [a]
4	-	S
11	+	MR-MS
18	+	MR
24	+	MR
32	+	MR/R
39	-	S
42	+	MR-MS
45	+	MR
51	+	MR-MS
58	-	S
69	-	S
70	-	S
74	-	S
76	-	S
80	+	MR-MS
CI 14035	+	MR
CSA	-	S

[a] Infection response: 'R' indicates resistant, 'MR' indicates moderately resistant, 'MS' indicates moderately susceptible, and 'S' indicates susceptible after Roelfs et al. (1992). When families were observed to be heterogeneous for infection response, the most common infection response was recorded, followed by a '/', and followed by the least common infection response.

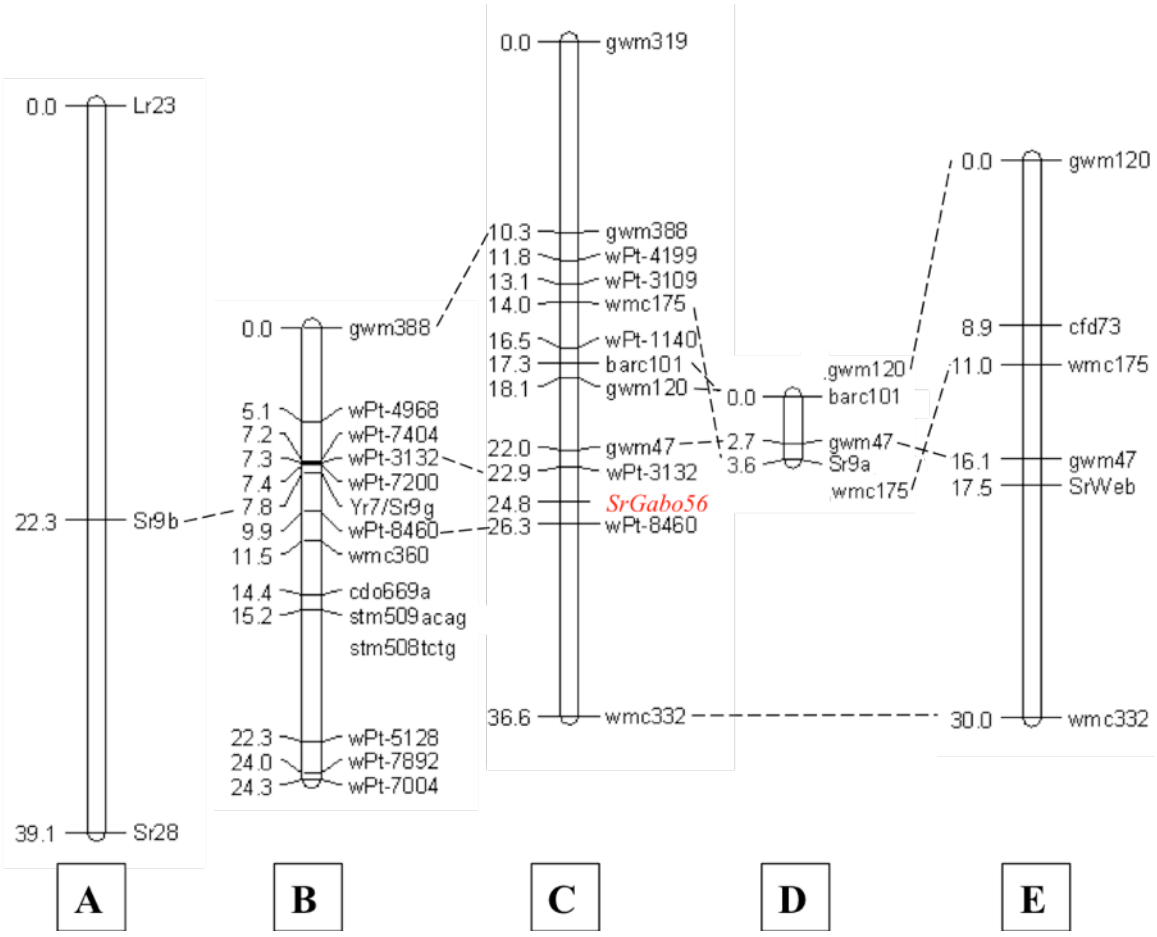

Figure 8.1. Genetic maps of chromosome 2B from our data and previously published studies: McIntosh, 1978 (A), Akbari et al., 2006 (B), Gabo 56/Chinese Spring (C), Tsilo et al., 2007 (D), and Hiebert et al., 2010 (E)

Chapter IX

Genetics and mapping of resistance to *Puccinia graminis* f. sp. *tritici* race TTKSK in SD 1691 wheat

Summary

Wheat stem rust, caused by *Puccinia graminis* f. sp. *tritici*, has been controlled the last several decades worldwide through the use of genetic resistance. Stem rust race TTKSK (Ug99), first reported in Uganda in 1999, threatens global wheat production because of its unique virulence combination. As the majority of the currently grown cultivars are susceptible to race TTKSK, sources of resistance need to be identified and characterized to facilitate their use in agriculture. South Dakota breeding line SD 1691 displayed resistance to race TTKSK in the international wheat stem rust nursery in Njoro, Kenya (trace to 10% severity and moderately resistant to moderately susceptible infection response). We evaluated the $F_{2:3}$ progeny of a cross between SD 1691 and susceptible LMPG-6 with race TTKSK. Seedling resistance in SD 1691 was inherited as a single dominant gene. Allelism and race-specificity tests indicated the stem rust resistance gene in SD 1691 is *Sr28*. Though monogenic lines with *Sr28* do not confer a high level of field resistance to race TTKSK, seedling and adult-plant screening of SD1691/LMPG-6 progeny suggested that the adult-plant resistance exhibited by SD 1691 is conferred by *Sr28*. We mapped *Sr28* to chromosome arm 2BL using DArT and SSR markers, the closest SSR marker being wmc332. Linkage analyses indicated that *Sr28* is independent of and linked in repulsion to *SrGabo56*, a recently described race TTKSK resistance gene in Gabo 56, also on chromosome arm 2BL. The identification of markers linked to *Sr28* and the linkage of *Sr28* and *SrGabo56* could facilitate the inheritance of these two genes

in breeding populations. Combining multiple resistance genes to race TTKSK in cultivars will likely be necessary to obtain durable resistance.

Introduction

Wheat stem rust, caused by *Puccinia graminis* f. sp. *tritici* (*Pgt*), is one of the most devastating diseases of wheat. During years conducive for disease development and presence of susceptible wheat cultivars, statewide yield losses reached 40-60% in North Dakota and Minnesota (Leonard, 2001). During the first two-thirds of the twentieth century, an emphasis on breeding resistant varieties of wheat coupled with the removal of the alternate host of stem rust, *Berberis vulgaris*, from areas where wheat is grown successfully resulted in the control of wheat stem rust in North America. Similarly, deploying resistant varieties of wheat worldwide in concurrence with the 'green revolution' was successful in preventing epidemics of stem rust for the last several decades (Singh et al., 2008).

Wheat stem rust has re-emerged as a major threat to global wheat production. In 1999 a race of *Pgt* was reported from Uganda with virulence to many of the wheat stem rust resistance genes currently being used in agriculture (Pretorius et al., 2000; Jin et al., 2007). This race, commonly known as Ug99, was characterized as race TTKSK based upon the North American differential set (*Pgt*-TTKSK; Jin et al., 2008). *Pgt*-TTKSK has been demonstrated to be virulent to nearly all Asian cultivars and to the majority of North American cultivars including 84% of the hard red spring wheat cultivars and breeding lines grown in the northern Great Plains of the United States, where stem rust epidemics have historically been problematic (Jin and Singh, 2006; Fetch, 2007; Singh et al., 2008). The majority of resistant cultivars in the United States were reported to possess resistance

genes *Sr24* and *Sr36* (Jin and Singh, 2006). Variants of *Pgt*-TTKSK have been detected with virulence on these genes, increasing the devastative potential of the *Pgt*-TTKSK complex of races (Jin et al., 2008; Jin et al., 2009). Since its discovery, *Pgt*-TTKSK and related races have been detected in Kenya, Ethiopia, Sudan, Yemen, Iran, and South Africa (Wanyera et al., 2006; Nazari et al., 2009; Pretorius et al., 2010).

Resistant varieties of wheat to *Pgt*-TTKSK and its dangerous variants are needed. Several resistance genes have been identified that are effective to *Pgt*-TTKSK (Jin et al., 2007). Most of these genes are introgressed from wild relatives of wheat and possess linkage to undesireable traits. In order to achieve elusive long-lasting resistance to *Pgt*-TTKSK, combinations of multiple genes will need to be deployed in cultivars. Combining multiple resistance genes resulted in the control of stem rust in North America for several decades (Kolmer et al., 1991). Identification of molecular markers linked to resistance genes could facilitate the combining of genes in breeding lines. The characterization of additional stem rust resistance genes effective to race TTKSK are needed in order to provide breeders with several genes for pyramiding in varieties.

Previous studies identified SD 1691 (CI 12499) as possessing seedling and adult plant resistance to race TTKSK (;3 to ; seedling infection type and trace to 10% severity and moderately resistant to moderately susceptible infection response in the field in Kenya; Figure 9.1; Chapter VI). SD 1691 is a South Dakota breeding line from the 1940's. Though SD 1691 displayed adult plant resistance to a bulk of stem rust isolates in a field nursery in Saint Paul, Minnesota (Chapter VI), it is susceptible to nearly all races screened at the seedling stage except races TTKSK and TTKST (*Sr24*-virulent variant of

Pgt-TTKSK). The genes conferring the adult plant resistance in SD 1691 to North American isolates are not known. Variety Hope, the source of an adult plant resistance gene to stem rust, *Sr2*, appears in the pedigree of SD 1691, and it is possible that *Sr2* is contributing to the unusually high level of adult plant resistance in SD 1691. Since SD 1691 was resistant to *Pgt*-TTKSK at the seedling stage, but not to most other races of stem rust, we suspected that SD 1691 might carry *Sr28*, which confers resistance to *Pgt*-TTKSK but very few other races of stem rust (Jin et al., 2007). The variety Ceres is in the pedigree of SD 1691 and Ceres is known to possess *Sr28* (McIntosh, 1978). We wanted to test the hypothesis that SD 1691 carries *Sr28*. Gene *Sr28* is located on chromosome 2BL, and previous studies demonstrated that a *Pgt*-TTKSK resistance gene in cultivar Gabo 56 exists on chromosome 2BL that is possibly a new allele of *Sr9* (Chapter VIII). The primary objectives of this research were to (1) determine the genetics of resistance to stem rust race TTKSK in SD 1691 and (2) map this resistance. We also wanted to test if (1) SD 1691 possesses *Sr28*, (2) seedling resistance in SD 1691 to corresponds to adult plant resistance, and (3) seedling resistance in SD 1691 is genetically independent of the new resistance gene previously described in cultivar Gabo 56 (Chapter VIII).

Materials and methods

Plant material and stem rust phenotyping

Seed of the cultivars SD 1691 (CI 12499; pedigree Hope/Reliance/Reward//Mercury) and Gabo 56 (CI 14035; pedigree Timstein/Kenya 58//Gabo) were obtained from the United States Department of Agriculture National Small Grains Collection (Aberdeen, ID). Line AD (W2691*5/Kota), a monogenic line with *Sr28*, was originally obtained from the University of Sydney (McIntosh, 1978). LMPG-6 is a selection of LMPG (Prelude/8*Marquis), a stem rust susceptible spring wheat developed by Knott (1990). A Line AD selection (referred to as W2691-*Sr28*) and LMPG-6 were stored at the United States Department of Agriculture Cereal Disease Laboratory (St. Paul, Minnesota). 104 $F_{2:3}$ families were developed from the cross between SD 1691 and susceptible LMPG-6. A total of 559 and 422 F_2 seeds were derived for allelism tests from crosses between SD 1691 and both W2691-*Sr28* and Gabo 56, respectively.

Progeny of all crosses were evaluated at the seedling stage with *Pgt*-TTKSK isolate 04KEN156/04 (synonymous with Ug99; Jin et al., 2007; Jin et al., 2008). For the SD 1691/LMPG-6 $F_{2:3}$ families, 15-20 seedlings were evaluated with *Pgt*-TTKSK. In order to evaluate seedlings with *Pgt*-TTKSK, dried urediniospores stored in gelatin capsules were obtained from a -80°C freezer, heat shocked in a 45°C water bath for 15 minutes, rehydrated for 2 to 4 hours in a chamber maintained at 80% relative humidity by a KOH solution (Rowell, 1984), and suspended in a light mineral oil (Soltrol 70,

ConocoPhillips Inc., Houston, TX) immediately before inoculation onto plants. Protocols for inoculating seedlings, incubating in dew chambers, and assessing disease 14 days after inoculation were followed as described by Jin et al. (2007). Stem rust infection types on the primary leaves of seedlings were classified on a 0-4 scale described by Stakman et al. (1962). Infection types '0' to '2', including ';3' mesothetic infection types, were considered low infection types, indicative of plant resistance and pathogen avirulence. Infection types '3' to '4' were considered high infection types corresponding to plant susceptibility. For the allelism tests, the numbers of resistant and susceptible plants were recorded for each population of F_2 individuals evaluated. For SD 1691/LMPG-6 progeny, $F_{2:3}$ families were classified as homozygous resistant, segregating, or homozygous susceptible. In each population, segregation of resistance was tested against expected ratios of resistant and susceptible plants by chi-square goodness-of-fit tests. Estimates of frequency of recombination and distance in centimorgans were calculated as in Kosambi (1944).

Sixteen $F_{2:3}$ SD 1691/LMPG-6 families were selected for *Pgt*-TTKSK evaluation at the adult plant stage. The families were selected based upon homogeneity for resistance or susceptibility at the seedling stage. Stem rust evaulation of adult plants was similar to seedling evaluations with the following exceptions: 4 plants grown in the same pot were evaluated for each family, plants were inoculated at heading, each family was inoculated with 15 mg of urediniospores of *Pgt*-TTKSK, disease assessments were made 21 days after inoculation, stem rust severities were evaluated on the 0-100% modified Cobb scale (Peterson et al., 1948), and stem rust infection responses were classified as

resistant (R), moderately resistant (MR), moderately susceptible (MS), susceptible (S), or combinations thereof (example: MR-MS) after Roelfs et al. (1992).

Molecular marker analyses

A total of 104 F_2 DNAs were extracted from the progeny of SD 1691/LMPG-6 corresponding to the $F_{2:3}$ families evaluated with *Pgt*-TTKSK. DNA was extracted for each F_2 plant using a CTAB method following Riede and Anderson (1996) with modifications by Liu et al. (2006) and further modifications including the use of a bead grinder (FastPrep®-24, MP Biomedicals, Inc.) to pulverize plant tissue. A total of 92 F_2 DNAs and DNA of the parents were genotyped with diversity arrays technology (DArT) markers according to Akbari et al. (2006). Preliminary mapping results indicated linkage between stem rust resistance segregating in the SD 1691/LMPG-6 population and DArT markers previously described on chromosome arm 2BL (Akbari et al., 2006). In order to identify microsatellite (SSR, simple sequence repeat) markers linked to the *Pgt*-TTKSK resistance trait, we screened the SD 1691, LMPG-6, and bulks of ten homozygous resistant or susceptible plants (Michelmore et al., 1991) with gwm, barc, and wmc microsatellite markers previously mapped to chromosome arm 2BL (Roder et al., 1998; Somers et al., 2004; Song et al., 2005).

The F_2 DNAs were then genotyped for the identified microsatellite markers. Microsatellite genotyping involved the amplification of the markers in 10 µL PCR reactions with 1 X PCR buffer (New England Biolabs, Inc. Beverley, MA), 0.125 mM dNTPs, 0.4 pmol forward primer, 0.3 pmol reverse primer, 3.0 pmol of M13 primer

(labeled with one of the following fluorescent dyes: 6-FAM, NEC, PET, and VIC), 0.05 units/µL Taq DNA polymerase (New England Biolabs), and 45 ng of genomic DNA. All PCR reactions were run on GeneAmp PCR system 9700 thermocyclers (Applied Biosystems, Foster City, CA) and denatured at 94ºC for 10 minutes, cycled through 94ºC for 1 minute, 50ºC for 1 minute, and 72ºC for 1 minute 40 times, kept at 72ºC for 5 minutes, and at 4ºC permanently. Four PCR reactions with different fluorescent dyes were multiplexed and 3 µL were combined with 0.14 µL size standard (GeneScan-500 LIZ®, Applied Biosystems) and 6.86 µL formamide (Hi-Di™, Applied Biosystems). The mixtures were denatured at 94ºC for 5 minutes and then placed on ice. Amplified fragments were analyzed using an ABI 3130xl Genetic Analyzer (Applied Biosystems) and GeneMapper software v3.7 (Applied Biosystems).

Mapping

For the DArT and microsatellite markers used in genotyping, chi-square tests were conducted to test for any linkage disequilibrium. A linkage map of the molecular markers and the stem rust resistance trait was constructed using Joinmap v4.0 (Stam, 1993; van Ooijen, 2006) with Kosambi's option for estimating distances (Kosambi, 1944), and a logarithm of odds value of 5.0.

Results

Stem rust phenotypic analyses and segregation of resistance

Both W2691-*Sr28* and SD 1691 displayed a ';3' seedling infection type to *Pgt*-TTKSK. Gabo 56 displayed a '2' to '2+' infection type and LMPG-6 displayed infection type '3+'. The $F_{2:3}$ progeny of SD 1691/LMPG-6 segregated for resistance to *Pgt*-TTKSK with resistant plants exhibiting ';3' to '3;' infection types and susceptible plants exhibiting infection types '3' to '4'. Segregation of resistance did deviate significantly from that expected for a single dominant gene with an unusually high number of segregating families recorded (Table 9.1). Segregation of the linked microsatellite marker also deviated significantly from the expected 1:2:1 ratio with a similar abundance of heterozygous F_2 plants (Table 9.1). These data suggest that the seedling resistance in SD 1691 is mediated by a single dominant gene at a locus in linkage disequilibrium. F_2 progeny of the cross between W2691-*Sr28* and SD 1691 did not segregate for resistance and all plants evaluated (559) had infection type ';3' (Table 9.2). These data indicate that the gene present in SD 1691 is *Sr28*. The F_2 progeny of the cross between SD 1691 and Gabo 56 displayed a range of infection types including ';3', '2', and '4' infection types (Figure 9.3). Out of 422 progeny screened, 4 F_2 plants were identified with susceptible infection types to *Pgt*-TTKSK (Table 9.2). This indicates that resistance in SD 1691 (*Sr28*) and resistance in Gabo 56 (*SrGabo56*) are not allelic and linked approximately 20 cM apart (Table 9.2).

Adult plant infection response of the 16 selected $F_{2:3}$ families derived from SD 1691/LMPG-6 were largely predictable based upon presence or absence of *Sr28* as determined by seedling infection types. Families without *Sr28* always exhibited susceptible infection responses and high severities of infection with the exception of family 9 with a 10% severity (Figure 9.2). This low severity relative to the other families without *Sr28* could be due to experimental error resulting in the family escaping much of the infection, presence of additional adult plant resistance genes, or misclassification of the absence of *Sr28*. Families postulated to possess *Sr28* all exhibited low severities and a low abundance of susceptible pustules if they were present (Figure 9.2). In this assay, SD 1691 displayed a 15 MR-MS adult plant reaction to *Pgt*-TTKSK.

Genetic mapping

Microsatellite marker wmc332 was identified as linked to *Sr28*. As mentioned earlier, wmc332 did deviate significantly from the expected segregation ratio indicating linkage disequilibrium (Table 9.1). Hybridization of F_2 DNAs to the DArT wheat array indicated the presence of 263 polymorphic DArT markers. Three markers were linked to *Sr28* (logarithm of odds value > 5.0; wPt-7004, wPt-5128, and wPt-7161). All of the DArT markers identified linked to *Sr28* hybridized with DNA inherited from LMPG-6. Markers wPt-5128 and wPt-7004 were previously mapped to chromosome arm 2BL (Akbari et al., 2006). The DArT markers did not deviate from expected segregation ratios (Table 9.1). The marker data for each $F_{2:3}$ individual and *Pgt*-TTKSK phenotypic classification used in mapping are available in Appendix VII.

Mapping the markers linked to *Sr28* identified wmc332 and wPt-7004 as flanking *Sr28* at 5.9 and 1.9 cM away respectively (Figure 9.4). Based upon marker order and genetic distances between markers, the mapping results demonstrated that *Sr28* is independent of *SrGabo56* (approximately 17.7 cM distal to *SrGabo56*; Figure 9.4). The distance estimate between *Sr28* and *SrGabo56* derived from comparing maps from chromosome 2BL (17.7 cM, Figure 9.4) is consistent with the distance estimate derived from segregation of resistance in the cross between SD 1691 and Gabo 56 (20.7 cM, Table 9.2).

Discussion

Segregation of resistance indicated that the single dominant gene, *Sr28*, confers the seedling resistance to *Pgt*-TTKSK in SD 1691. Evaluation of selected families with *Pgt*-TTKSK at the adult plant stage indicated that *Sr28* also confers resistance to *Pgt*-TTKSK at the adult plant stage in SD 1691. This finding is significant because monogenic lines with *Sr28* did not display an adequate level of adult plant resistance to *Pgt*-TTKSK in the field in Njoro, Kenya (Jin et al., 2007). Three possible reasons for the higher level of adult plant resistance exhibited by SD 1691 compared to W2691-*Sr28* are (1) the genetic background of SD 1691 enhances the effectiveness of *Sr28*, (2) SD 1691 possesses an allele of *Sr28* that is more effective to TTKSK than the allele in W2691-*Sr28*, and (3) SD 1691 possesses partial resistance to *Pgt*-TTKSK that is complementary to *Sr28*. Detailed studies evaluating the adult plant resistance of recombinant inbred lines derived from crosses between SD 1691 and both LMPG-6 and W2691-*Sr28* could be constructed to test these hypotheses. Regardless of the specific mechanisms involved, we have demonstrated that *Sr28* can be used as an effective source of adult plant resistance to *Pgt*-TTKSK.

We identified molecular markers linked to *Sr28* on chromosome arm 2BL (Table 9.1). Though only one microsatellite marker was identified as linked to *Sr28*, three DArT markers were identified. Further studies are currently in progress in our laboratory to develop PCR-based markers from the sequences of the linked DArT markers. PCR-based markers are necessary for marker-assisted selection of *Sr28*. The use of wmc332

proximal to *Sr28* with a PCR-based marker distal to *Sr28* could provide breeders with the tools to successfully select for *Sr28* in breeding populations with a high degree of certainty.

Segregation of resistance indicated that *Sr28* is linked to *SrGabo56* (approximately 20.7 cM; Table 9.2). Comparison of the map created in this study with previously produced maps of chromosome 2B show consistent marker order and reasonably consistent genetic distances between markers (Figure 9.4). McIntosh (1978) estimated the distance between *Sr9b* and *Sr28* to be 16.8 cM. This distance is consistent with our estimate of the distance between *Sr28* and *SrGabo56*; it is possible that *SrGabo56* is an allele of the *Sr9* locus (Chapter VIII). Akbari et al. (2006) found that wPt-7004 was distal to wPt-5128 in contrast to our results. Since these markers are separated by small distances and they are dominant markers, this inconsistency is not surprising. Similarly, wmc175 is inconsistent in marker order across the various maps of chromosome 2BL and is a dominant marker (Figure 9.4).

The demonstration of linkage of two *Pgt*-TTKSK resistance genes (*Sr28* and *SrGabo56*) in hard red spring wheat germplasm is significant for global wheat production. The availability of effective resistance genes to *Pgt*-TTKSK in hard red spring wheat germplasm is limited (Jin and Singh, 2006). *Sr28* and *SrGabo56* provide hard red spring wheat breeders with additional options in breeding for resistance. The linkage of these two genes will facilitate their pyramiding in breeding populations. One of the major limitations to pyramiding multiple genes is the low probability of obtaining desirable combinations. We are currently in the process of identifying and increasing

seed of progeny of the cross between SD 1691 and Gabo 56 that have *Sr28* and *SrGabo56* in coupling. These lines will be available for distribution once they are identified and increased. The production of lines with *Sr28* and *SrGabo56* in coupling and the development of accessible molecular markers linked to this linkage group will facilitate the rapid introgression of a two-gene pyramid derived from hard red spring wheat germplasm.

Table 9.1. Segregation of *Pgt*-TTKSK resistance and linked markers among F_2 individuals or $F_{2:3}$ families used for mapping

Marker/Gene	a[a]	h	b	c	d	Total	X^{2} [b]	*P* value
wmc332	15	50	14	2	2	83	10.82	4.47E-03
Sr28	20	67	17	-	-	104	7.63	0.02
wPt-7004	20	-	-	67	-	87	0.19	0.66
wPt-5128	22	-	-	64	-	86	0.02	0.90
wPt-7161	20	-	-	62	-	82	0.02	0.90

[a] 'a' refers to homozygous for the SD 1691 allele, 'h' refers to heterozygous, 'b' refers to homozygous for the LMPG-6 allele, 'c' refers to either heterozygous or homozygous LMPG-6, and 'd' refers to heterozygous or homozygous SD 1691.

[b] X^2 values were calculated for testing 1:2:1 segregation for codominant markers, wmc332 and *Sr28* (2 df) or 3:1 segregation for dominant markers (1 df). Occasional inidividuals classified as 'c' or 'd' were not included in calculaiton of X^2 values for codominant markers.

Table 9.2. Segregation of resistance to *Pgt*-TTKSK in F_2 plants of allelism tests

Parent 1	Parent 2	Res.	Sus.	Ratio	X^2	*P* value	r[a]	cM
SD 1691	W2691-*Sr28*	559	0	15:1	37.27	1.03E-09	0	0
SD 1691	Gabo 56	418	4	15:1	20.25	6.78E-06	0.196	20.7

[a] Rough distance estimates of 'r' and 'cM' (Kosambi's distance estimate used; Kosambi, 1944) were calculated based upon the available data.

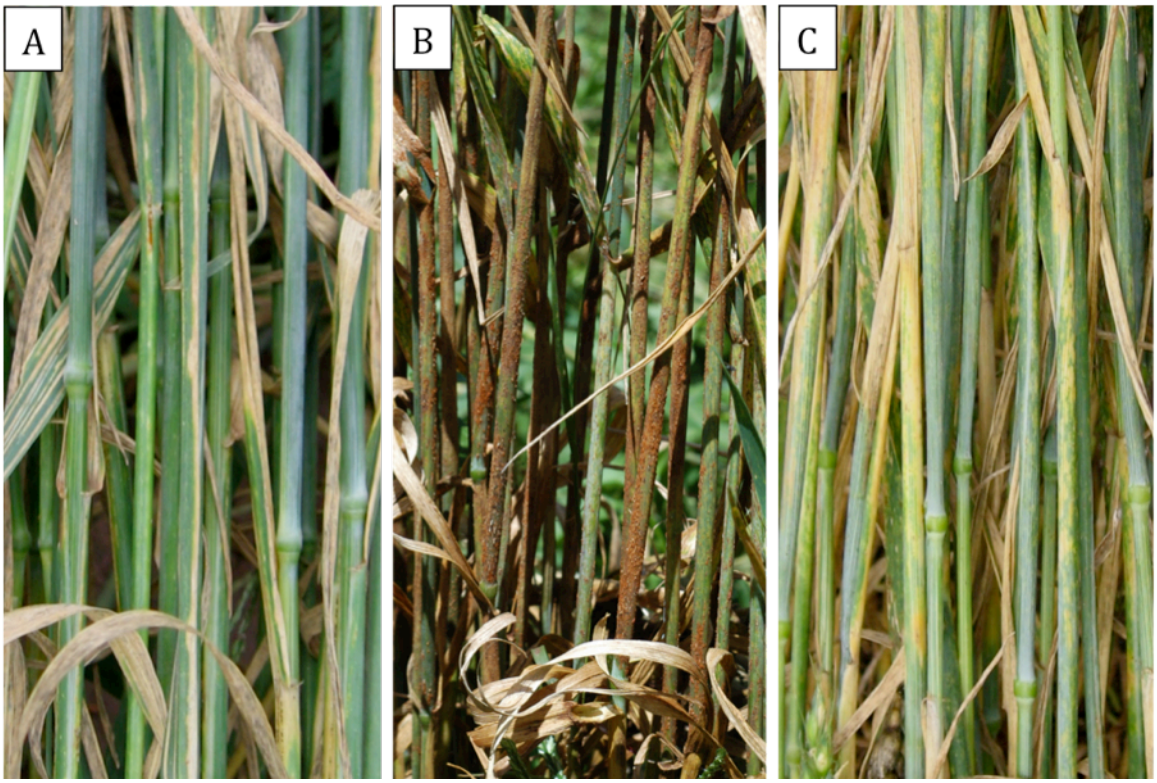

Figure 9.1. Adult plant reaction to stem rust in Njoro Kenya (2009) of SD 1691 (A), LMPG-6 (B), and Gabo 56 (C)

$F_{2:3}$ Family	*Sr28*	Severity[b], IR[a]
2	-	60 S
7	-	60 S
9	-	10 S
10	-	60 S-MS
12	-	70 S
14	-	70 S-MS
15	-	80 S-MS
16	-	60 S
20	-	40 MS-S
25	+	T S
37	+	T R-MS
38	+	5 R, T MS
40	+	5 R-S
42	+	T S
51	+	15 S-MS-R
54	+	5 R-MS

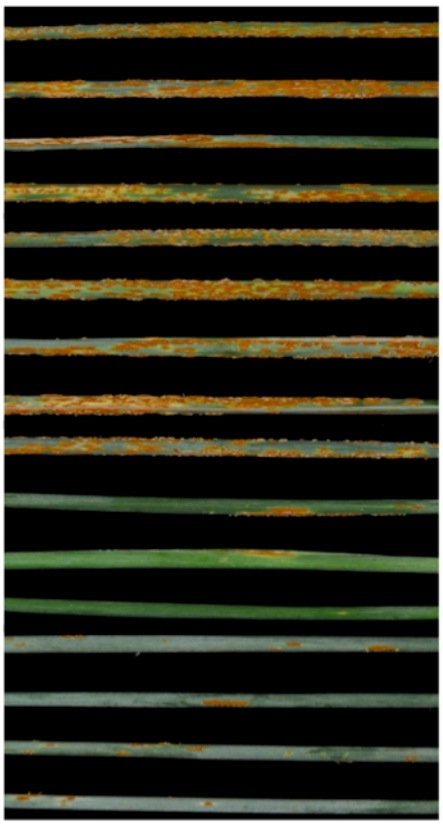

Figure 9.2. Adult plant severity and infection responses (IR) of selected homozygous resistant or susceptible $F_{2:3}$ families

[a] Infection response: 'R' indicates resistant, 'MR' indicates moderately resistant, 'MS' indicates moderately susceptible, and 'S' indicates susceptible after Roelfs et al. (1992).

[b] Severity was assessed on the 0-100% modified Cobb scale described by Peterson et al. (1948). 'T' indicates trace or less than 5% severity.

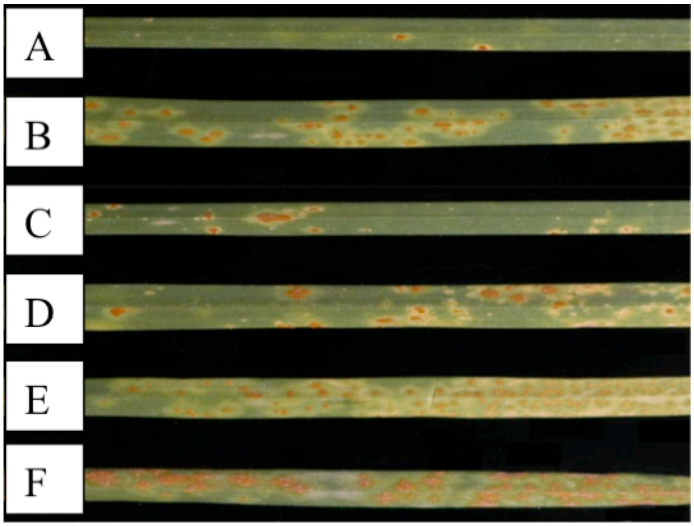

Figure 9.3. *Pgt*-TTKSK seedling infection types of SD 1691 (A), Gabo 56 (B), resistant SD 1691/Gabo 56 F_2 progeny (C-E), and a susceptible SD 1691/Gabo 56 F_2 seedling (F)

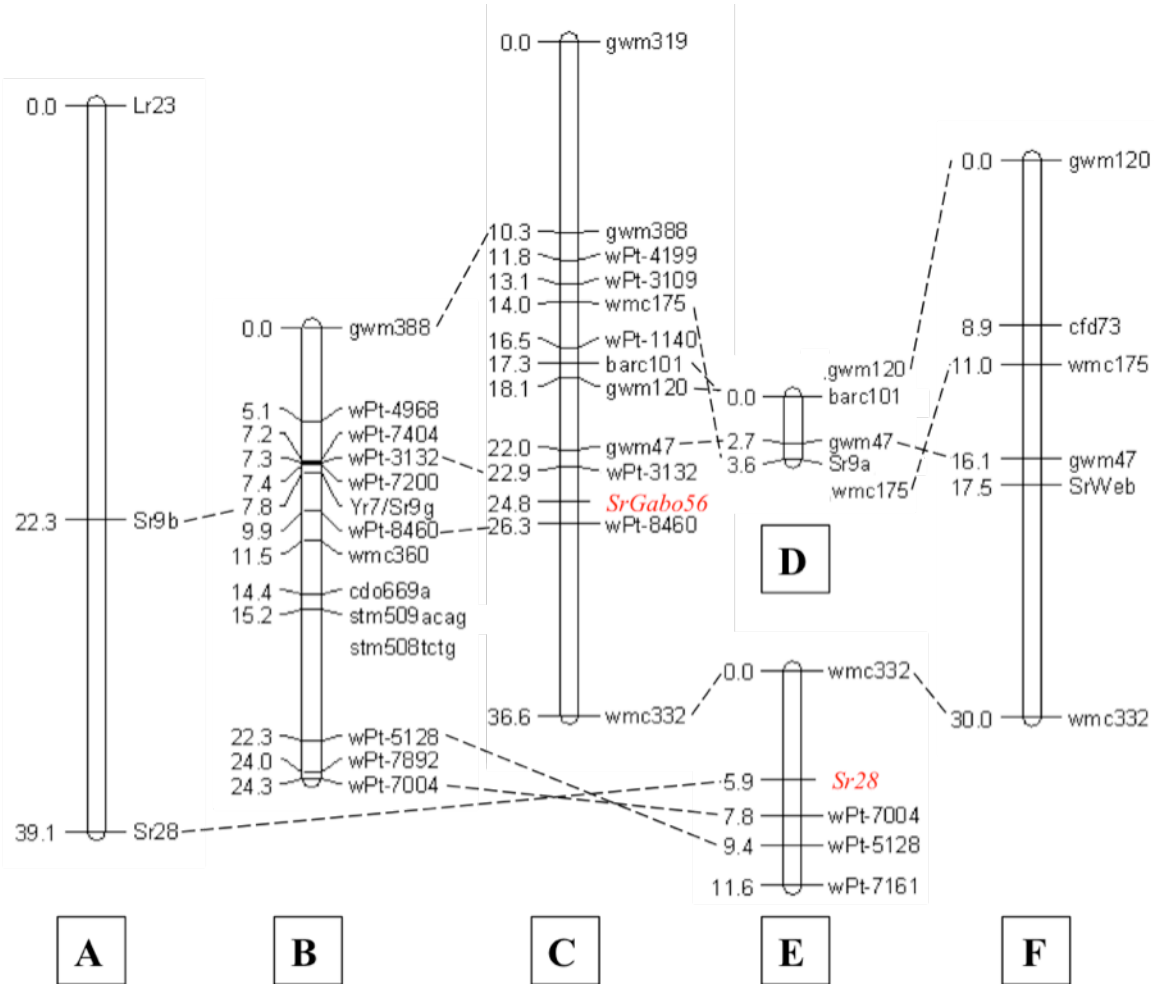

Figure 9.4. Genetic maps of chromosome arm 2BL or 2B from our data and previously published studies: McIntosh, 1978 (A), Akbari et al., 2006 (B), Gabo 56/Chinese Spring (described in Chapter 8) (C), Tsilo et al., 2007 (D), SD 1691/LMPG-6 (E), and Hiebert et al., 2010 (F)

Bibliography

Admassu, B., V. Lind, W. Friedt, and F. Ordon. 2009. Virulence analysis of *Puccinia graminis* f. sp. *tritici* populations in Ethiopia with special consideration of Ug99. Plant Pathology 58:362-369.

Akbari, M., P. Wenzl, V. Caig, J. Carling, L. Xia, S. Yang, G. Uszynski, V. Mohler, A. Lehmensiek, H. Kuchel, M. J. Hayden, N. Howes, P. Sharp, P. Vaughan, B. Rathmell, E. Huttner, and A. Kilian. 2006. Diversity arrays technology (DArT) for high-throughput profiling of the hexaploid wheat genome. Theor. Appl. Genet. 113:1409-1420.

Assefa, S. and H. Fehrmann. 2004. Evaluation of *Aegilops tauschii* Coss. for resistance to wheat stem rust and inheritance of resistance genes in wheat. Genetic Resources and Crop Evolution 51:663-669.

Bai, J., S. H. Choi, G. Ponciano, H. Leung, and J. E. Leach. 2000. *Xanthomonas oryzae* pv. *oryzae* avirulence genes contribute differently and specifically to pathogen aggressiveness. Molecular Plant-Microbe Interactions 13:1322-1329.

Bonman, J. M., H. E. Bockelman, Y. Jin, R. J. Hijman, and A. I. N. Gironella. 2007. Geographic distribution of stem rust resistance in wheat landraces. Crop Sci. 47:1955-1963.

Chu, C.-G., J. D. Faris, T. L. Friesen, and S. S. Xu. 2006. Molecular mapping of hybrid necrosis genes *Ne1* and *Ne2* in hexaploid wheat using microsatellite markers. Theoretical and Applied Genetics 112:1374-1381.

Fetch, T. Jr. 2007. Virulence of stem rust race TTKS on Canadian wheat cultivars. Can. J. Plant Pathol. 29:441.

Forsyth, F. R. 1956. Interaction of temperature and light on the seedling reaction of McMurachy wheat to race 15B of stem rust. Canadian Journal of Botany 34:745-749.

Friesen, T. L., S. S. Xu, and M. O. Harris. 2008. Stem rust, tan spot, Stagonospora nodorum blotch, and hessian fly resistance in Langdon durum-*Aegilops tauschii* synthetic hexaploid wheat lines. Crop Science 48:1062-1070.

Gerechter-Amitai, Z. K., I. Wahl, A. Vardi, and D. Zohary. 1971. Transfer of stem rust seedling resistance from wild diploid einkorn to tetraploid durum wheat by means of a triploid hybrid bridge. Euphytica 20:281-285.

Heun, M., S. Haldorsen, and K. Vollan. 2008. Reassessing domestication events in the Near East: Einkorn and *Triticum urartu*. Genome 51:444-451.

Hiebert, C. W., T. G. Fetch, Jr., and T. Zegeye. 2010. Genetics and mapping of stem rust resistance to Ug99 in the wheat cultivar Webster. Theor. Appl. Genet. 121:65-69.

Huerta-Espino, J. 1992. Analysis of wheat leaf and stem rust virulence on a worldwide basis. PhD Thesis, University of Minnesota, USA.

Jin, Y. and R. P. Singh. 2006. Resistance in U.S. wheat to recent eastern African isolates of *Puccinia graminis* f. sp. *tritici* with virulence to resistance gene *Sr31*. Plant Disease 90:476-480.

Jin, Y., R. P. Singh, R. W. Ward, R. Wanyera, M. Kinyua, P. Njau, T. Fetch, Z. A. Pretorius, and A. Yahyaoui. 2007. Characterization of seedling infection types

and adult plant infection responses of monogenic *Sr* gene lines to race TTKS of *Puccinia graminis* f. sp. *tritici*. Plant Disease 91:1096-1099.

Jin., Y., B. J. Steffenson, and T. G. Fetch. Jr. 1994. Sources of resistance to pathotype QCC of *Puccinia graminis* f. sp. *tritici* in Barley. Crop Sci. 34:285-288.

Jin, Y., L. J. Szabo, Z. A. Pretorius, R. P. Singh, R. Ward, and T. Fetch Jr. 2008. Detection of virulence to resistance gene *Sr24* within race TTKS of *Puccinia graminis* f. sp. *tritici*. Plant Disease 92:923-926.

Jin, Y., L. J. Szabo, M. N. Rouse, T. Fetch Jr., Z. A. Pretorius, R. Wanyera, and P. Njau. 2009. Detection of virulence to resistance gene *Sr36* within the TTKS race lineage of *Puccinia graminis* f. sp. *tritici*. Plant Disease 93:367-370.

Jing, H.-C., C. Bayon, K. Kanyuka, S. Berry, P. Wenzl, E. Huttner, A. Kilian, and K. E. Hammond-Kosack. 2009. DArT markers: diversity analyses, genomes comparison, mapping and integration with SSR markers in *Triticum monococcum*. BMC Genomics 10:458.

Johnson, R. 1984. A critical analysis of durable resistance. Annual Review of Phytopathology 22:309-330.

Kerber, E. R. and P. L. Dyck. 1973. Inheritance of stem rust resistance transferred from diploid wheat (*Triticum monococcum*) to tetraploid and hexaploid wheat and chromosome location of the gene involved. Can. J. Genet. Cytol. 15:397-409.

Kerber, E. R. and P. L. Dyck. 1979. Resistance to stem and leaf rust of wheat in *Aegilops squarrosa* and transfer of a gene for stem rust resistance to hexaploid wheat. P. 358-364. *In* S. Ramanujam (ed.) Proc. Int. Wheat Genet. Symp., 5th, New Delhi,

India. 23-28 Feb. 1978. Indian Society of Genetics and Plant Breeding, New Delhi, India.

Kihara, H. 1944. Discovery of the DD analyzer, one of the ancestors of *Triticum vulgare*. Agriculture and Horticulture 19:889-890.

Knott, D. R. 1982. Multigenic inheritance of stem rust resistance in wheat. Crop Science 22:393-399.

Knott, D. R. 1988. Using polygenic resistance to breed for stem rust resistance in wheat. *In: Breeding strategies for resistance to the rusts of wheat*. Eds. N. W. Simmonds and S. Rajaram. CIMMYT. Mexico, D. F.

Knott, D. R. 1990. Near-isogenic lines of wheat carrying genes for stem rust resistance. Crop Sci. 30:901-905.

Kolmer, J. A., P. L. Dyck, and A. P. Roelfs. 1991. An appraisal of stem and leaf rust resistance in North American hard red spring wheats and the probability of multiple mutations to virulence in populations of cereal rust fungi. Phytopathology 81:237-239.

Kosambi, D. D. 1944. The estimation of map distances from recombination values. Ann. Eugen. 12:172-175.

Large, E. C. 1954. Growth stages in cereals. Plant Pathology 3:128-129.

Leach, J. E., C. M. Vera Cruz, J. Bai, and H. Leung. 2001. Pathogen fitness penalty as a predictor of durability of disease resistance genes. Annual Review of Phytopathology 39:187-224.

Leonard, K. J. 2001. Stem rust – future enemy? pp 119-146. *In: Stem rust of wheat: from ancient enemy to modern foe. Ed. P. D. Peterson.* APS Press, St. Paul, Minnesota.

Line, R. F. and C. S. Griffith. 2001. Research on the epidemiology of stem rust of wheat during the cold war. pp 83-118. *In: Stem rust of wheat: from ancient enemy to modern foe. Ed. P. D. Peterson.* APS Press, St. Paul, Minnesota.

Liu, S., L.-X. Yu, R. P. Singh, Y. Jin, M. E. Sorrells, and J. A. Anderson. 2010. Diagnostic and co-dominant PCR markers for wheat stem rust resistance genes *Sr25* and *Sr26*. Theor. Appl. Genet. 120:691-697.

Liu, S., X. Zhang, M. O. Pumphrey, R. W. Stack, B. S. Gill, and J. A. Anderson. 2006. Complex microlinearity among wheat, rice, and barley revealed by fine mapping of the genomic region harboring a major QTL for resistance to fusarium head blight in wheat. Funct. Integr. Genomics 6:83-89.

Marais, G. F., W. G. Wessels, M. Horn, and F. du Toit. 1998. Association of a stem rust resistance gene (*Sr45*) and two Russian wheat aphid resistance genes (*Dn5* and *Dn7*) with mapped structural loci in common wheat. S. Afr. J. Plant Soil 15:67-71.

McIntosh, R. A. 1972. Cytogenetical studies in wheat: VI. Chromosome location and linkage studies involving *Sr13* and *Sr8* for reaction to *Puccinia graminis* f. sp. *tritici*. Aust J Biol Sci 25:765-763.

McIntosh R. A. 1978. Cytogenetic studies in wheat X. Monosomic analysis and linkage studies involving genes for resistance to *Puccinia graminis* f. sp. *tritici* in cultivar Kota. Heredity 41:71-82.

McIntosh, R. A., Dyck, P. L., The, T. T., Cusick, J., and Milne, D. L. 1984. Cytogenetical studies in wheat XIII. *Sr35* – a third gene from *Triticum monococcum* for resistance to *Puccinia graminis tritici*. Z. Pflanzenzuchtg 92:1-14.

McIntosh, R. A., C. R. Wellings, and R. F. Park. 1995. Wheat rusts: An atlas of resistance genes. CSIRO Publications, East Melbourne, Australia, pp 83-148.

McIntosh, R. A., Y. Yamazaki, J. Dubcovsky, W. J. Rogers, C. F. Morris, D. Somers, R. Appels, and K. M. Devos. 2008. Catalogue of gene symbols for wheat. In: McIntosh R. A. (ed), Gene symbols. http://wheat.pw.usda.gov/GG2/Triticum/wgc/2008/GeneSymbol.pdf

Michelmore, R. W., I. Paran, and R. V. Kesseli. 1991. Identification of markers linked to disease-resistance genes by bulked segregant analysis: a rapid method to detect markers in specific genomic regions by using segregating populations. Proc. Natl. Acac. Sci. USA 88:9828-9832.

Moghaddam, M., B. Ehdaie, and J. G. Waines. 2000. Genetic diversity in populations of wild diploid wheat *Triticum urartu* Tum. ex. Gandil. revealed by isozyme markers. Genetic Resources and Crop Evolution 47:323-334.

Mundt, C. C. 1990. Probability of multiple virulence and durability of resistance gene pyramids. Phytopathology 80:221-223.

Mundt, C. C. 1991. Probability of mutation to multiple virulence and durability of resistance gene pyramids: further comments. Phytopathology 81:240-242.

Nazari, K., M. Mafi, A. Yahyaoui, R. P. Singh, and R. F. Park. 2009. Detection of wheat stem rust (*Puccinia graminis* f. sp. *tritici*) race TTKSK (Ug99) in Iran. Plant Dis. 93:317.

Njau, P. N., Y. Jin, J. Huerta-Espino, B. Keller, and R. P. Singh. 2010. Identification and evaluation of sources of resistance to stem rust race Ug99 in wheat. Plant Dis. 94:413-419.

Ogbonnaya, F. C., M. Imtiaz, H. S. Bariana, M. McLean, M. M. Shankar, G. J. Hollaway, R. M. Trethowan, E. S. Lagudah, and M. van Ginkel. 2008. Mining synthetic hexaploids for multiple disease resistance to improve bread wheat. Australian Journal of Agricultural Research 59:421-431.

Olson, E. L., G. Brown-Geudira, D. S. Marshall, Y. Jin, M. Mergoum, I. Lowe, and J. Dubcovsky. 2010. Genotyping of U.S. wheat germplasm for presence of stem rust resistance genes *Sr24*, *Sr36*, and $Sr1RS^{Amigo}$. Crop Sci. 50:668-675.

Olson, E., G. Brown-Geudira, D. Marshall, E. Stack, R. L. Bowden, Y. Jin, M. Rouse, and M. O. Pumphrey. 2010. Development of wheat lines having a small introgressed segment carrying stem rust resistance gene *Sr22*. Crop Science *in press.*

Peterson, R. F., Campbell, A. B., and Hannah, A. E. 1948. A diagrammatic scale for estimating rust intensity of leaves and stem of cereals. Can. J. Res. Sect. C 26:496-500.

Pretorius, Z. A., C. M. Bender, B. Visser, and T. Terefe. 2010. First report of a *Puccinia graminis* f. sp. *tritici* race virulent to the *Sr24* and *Sr31* wheat stem rust resistance genes in South Africa. Plant Dis. 94:784.

Pretorius, Z. A., R. P. Singh, W. W. Wagoire, and T. S. Payne. 2000. Detection of virulence to wheat stem rust resistance gene *Sr31* in *Puccinia graminis* f. sp. *tritici* in Uganda. Plant Dis. 84:203.

Riede, C. R., and J. A. Anderson. 1996. Linkage of RFLP markers to an aluminum tolerance gene in wheat. Crop Sci. 36:905-909.

Roder, M. S., V. Korzun, K. Wendehake, J. Plaschke, M. Tixier, P. Leroy, and M. W. Ganal. 1998. A microsatellite map of wheat. Genetics 149:2007-2023.

Roelfs, A. P. 1978. Estimated losses caused by rust in small grain cereals in the United States: 1918-76. U.S. Dep. Agric., Agricultural Research Service, Miscellaneous Publication 1363.

Roelfs, A. P., D. L. Long, and J. J. Roberts. 1993. Races of *Puccinia graminis* in the United States during 1990. Plant Dis. 77:125-128.

Roelfs, A. P. and J. W. Martens. 1988. An international system of nomenclature for *Puccinia graminis* f. sp. *tritici*. Phytopathology 78:526-533.

Roelfs, A. P. and McVey, D. V.. 1979. Low infection types produced by *Puccinia graminis* f. sp. *tritici* and wheat lines with designated genes for resistance. Phytopathology 69:722-730.

Roelfs, A. P., Singh, R. P., and Saari, E. E. 1992. Rust diseases of wheat: concepts and methods of disease management. CIMMYT, Mexico, D.F.

Rouse, M. N., S. Stoxen, X. Chen, L. J. Szabo, and Y. Jin. 2009. Diverse stem rust races found in a single field in Washington, USA. Plant Dis. 99:S111.

Rowell, J. B. 1984. Controlled infection by *Puccinia graminis* f. sp. *tritici* under artificial conditions. Pages 292-332 in: The Cereal Rusts, Vol. 1. Origins, Specificity, Structure, and Physiology. W. R. Bushnell and A. P. Roelfs, eds. Academic Press, Orlando, FL.

Schafer, J. F. and A. P. Roelfs. 1985. Estimated relation between numbers of urediniospores of *Puccinia graminis* f. sp. *tritici* and rates of occurrence of virulence. Phytopathology 75:749-750.

Simons, K., Z. Abate, S. Chao, W. Zhang, M. Rouse, Y. Jin, E. Elias, and J. Dubcovsky. 2010. Genetic mapping of stem rust resistance gene *Sr13* in tetraploid wheat (*Triticum turgidium* spp. *Durum* L.). Theor. Appl. Genet. *In Review.*

Singh, R. P., D. P. Hodson, J. Huerta-Espino, Y. Jin, P. Njau, R. Wanyera, S. A. Herrera-Foessel, and R. W. Ward. 2008. Will stem rust destroy the world's wheat crop? Advances in Agronomy 98:271-309.

Singh, R. P., D. P. Hodson, Y. Jin, J. Huerta-Espino, M. G. Kinyua, R. Wanyera, P. Njau, and R. W. Ward. 2006. Current status, likely migration and strategies to mitigate the threat to wheat production from race Ug99 (TTKS) of stem rust pathogen. CAB Reviews 54:1-13.

Singh, R. P., J. Huerta-Espino, and H. M. William. 2005. Genetics and breeding for durable resistance to leaf and stripe rusts in wheat. Turkish Journal of Agriculture and Forestry 29:121-127.

Somers, D. J., P. Isaac, and K. Edwards. 2004. A high density microsatellite consensus map for bread wheat (*Triticum aestivum* L.). Theor. Appl. Genet. 109:1105-1114.

Song, Q. J., J. R. Shi, S. Singh, E. W. Fickus, J. M. Costa, J. Lewis, B. S. Gill, R. Ward, and P. B. Cregan. 2005. Development and mapping of microsatellite (SSR) markers in wheat. Theor. Appl. Genet. 110:550-560.

Stakman, E. C., Steward, D. M., and Loegering, W. Q. 1962. Identification of physiologic races of *Puccinia graminis* var. *tritici*. United States Department of Agriculture Agricultural Research Service E-617.

Stam, P. 1993. Construction of integrated genetic linkage maps by means of a new computer package: JoinMap. Plant J. 3:739-744.

The, T. T. 1973a. Chromosome location of genes conditioning stem rust resistance transferred from diploid to hexaploid wheat. Nature New Biology 241:256.

The, T. T. 1973b. Transference of resistance to stem rust from *Triticum monococcum* L. to hexaploid wheat. Ph.D. Thesis, The University of Sydney.

Tsilo, T. J., Y. Jin, and J. A. Anderson. 2007. Microsatellite markers linked to stem rust resistance allele *Sr9a* in wheat. Crop Sci. 47:2013-2020.

Tsilo, T. J., S. Chao, Y. Jin, and J. A. Anderson. 2009. Identification and validation of SSR markers linked to the stem rust resistance gene *Sr6* on the short arm of chromosome 2D in wheat. Theor. Appl. Genet. 118:515-524.

Tsilo, T. J., Y. Jin, and J. A. Anderson. 2008. Diagnostic microsatellite markers for the detection of stem rust resistance gene *Sr36* in diverse genetic backgrounds of wheat. Crop Sci. 48:253-261.

Van Der Planck, J. E. 1968. Disease Resistance in Plants. Academic Press, New York, New York.

van Ooijen, J. W. 2006. JoinMap 4.0: Software for the calculation of genetic linkage maps in experimental populations. Kyazma B. V., Wageningen, Netherlands.

Visser, B., L. Herselman, and Z. A. Pretorius. 2009. Genetic comparison of Ug99 with selected South African races of *Puccinia graminis* f. sp. *tritici*. Molecular Plant Pathology 10:213-222.

Wanyera, R., M. G. Kinyua, Y. Jin, and R. P. Singh. 2006. The spread of stem rust caused by *Puccinia graminis* f. sp. *tritici*, with virulence on *Sr31* in wheat in eastern Africa. Plant Dis. 90:113.

Wanyera, R., J. K. Macharia, S. M. Kilonzo, and J. W. Kamundia. 2009. Foliar fungicides to control wheat stem rust, race TTKS (Ug99), in Kenya. Plant Dis. 93:929-932.

Watson, I. A., and Luig, N. H. 1963. The classification of *Puccinia graminis* var. *tritici* in relation to breeding resistant varieties. Proc. Linn. Soc. N. S. W. 88:235-258.

Watson, I. A., and Luig, N. H. 1968. Progressive increase in virulence in *Puccinia graminis* f. sp. *tritici*. Phytopathology 58: 70-73.

Yu, L. X., S. Liu, J. A. Anderson, R. P. Singh, Y. Jin, J. Dubcovsky, G. Brown-Geudira, S. Bhavani, A. Morgounov, Z. He, J. Huerta-Espino, and M. E. Sorrells. 2010. Haplotype diversity of stem rust resistance loci in uncharacterized wheat lines. Mol. Breeding DOI 10.1007/s11032-010-9403-7.

APPENDICES

List of Appendices

APPENDIX I: *Aegilops tauschii* screening data

WGGRC accession	GRIN accession	TRTTF	TTKSK	TTTTF	QTHJC	RKQQC	TPMKC
TA 1577		33+	2	3	;,1+	2+,3	1+
TA 1579		4	2/3+	4	3	3+,4	3-
TA 1580		4	4	4	3=	3+	3=
TA 1585	PI 486268	3+	3+	;,1,1+	;,1	2+,3	3
TA 1586	PI 486269	4	3+	4	2++	3+,4	3+
TA 1590	PI 486273	4	3	4	3	3	3
TA 1595		4	4	4	-	3=	3
TA 1596		3+	4	4	3	3+,4	3
TA 1597	PI 603221	4	4	4	3=	3+,4	3
TA 1598	PI 603222	4	4	4	3+,4	3-	3-
TA 1601		4	4	4	3	3++	3
TA 1602		4	4	4	2+	3=	3-
TA 1603		4	3+	4	3	3=	3
TA 1605		2,3-	;,2-	3+	2,=2	3-	2-
TA 1606	PI 506403	-	;,2-,2	;,2-	-	1,1-	0
TA 1612		3,3+/2,3	4	;,2-,3+	2=	3+,4	3+,4
TA 1613		3,3+	2	4	1,2N	2++	1+
TA 1615		;1	2-	;,2-,3-	;,1-	3,3=	1+
TA 1620	PI 317398	4	3,3+	4	3	3++	3
TA 1634	PI 170290	4	4	4	3-	3	3
TA 1635		;,1N/;,1,3-N	;,1	;,1N	;,1-	2	2-,1
TA 1639		4	3	4	3+,4	3-	3
TA 1640		4	2,3	4	3	3-	3
TA 1641	PI 603226	4	4	4	3+	3 LIF	3
TA 1642	PI 603227	;,1	;,1	3	1-	1,1+ LIF	;,1-
TA 1643		2,3	3+	2-,3+	2=	4	3-
TA 1644		;,2	2-,2	;,2-	1+	0;,1	1-
TA 1645		;,1,2-	;,2-	3+	2,2+ LIF	0	2-/3- LIF
TA 1649		3+	;,2-	3,3+	;,1+	0;	1=
TA 1650		4	2,3	4	3=	3-	2+
TA 1651	PI 603228	2,3	2-,2	;,2-/3+	0;	2+C LIF	2,2-
TA 1652		4	4	4	3,3+	3+,4	3
TA 1653		4	3	;,1,3+	2=	3	3
TA 1656		3	2,3	3,3+	-	2+,3	2+
TA 1657		3+	3+	4	3	3	3+
TA 1660	PI 603229	4	2	;,2-,3+	;,2=	3+,4	2+,3
TA 1661	PI 603256	2,3,;,3+	;	3,3+/2,-3	;,1	;,1-	;,1
TA 1662	PI 603230	;,1	2-	;,1,2-,3	0;	3= LIF	3=
TA 1665	PI 603231	3+	2	;,1,2-,3	;,1-	0	3=
TA 1666	PI 603232	2,2+	;,1,2-	;,1,2-	-	-	1,1+
TA 1667		4	3,3+	;,1,2-,3-	2=	3,2-	2+,3
TA 1668		;,1/;,1,3-	;	;,1,2-	;,1	3	2-
TA 1670	PI 603234	2,3	2,3	3+	2,2+	2+C LIF	;,1

APPENDIX I continued

WGGRC accession	GRIN accession	TRTTF	TTKSK	TTTTF	QTHJC	RKQQC	TPMKC
TA 1671	PI 603235	3,3+	2	4	-	0	2- LIF
TA 1672		1,2	;,2=	1,2-,3	2=	2,2+	0
TA 1673		1,2-	2-	1,2-	2=	2,2+	1,1+
TA 1675	PI 603236	;,1,2	;,1,2-	;,1,2-,3-	;,1	;,1-	2-
TA 1676		4	3	3+	4	3+	3-
TA 1677		4	4	1,2-,3	1	3+,4	2++
TA 1678		4	4	1,2-,3-	1	3+,4	3=
TA 1680		4	4	3+	2	2+,3	2+,3
TA 1681		4	2,2+/3+	3+	3-	3+,4	3=
TA 1682	PI 603237	4	3+	1,2-,3+	2-	3-	3-
TA 1683	PI 603238	4	4	1,3-/4	3/2=	3	3-
TA 1685	PI 603239	;,3+/4	;,2-/;,2-,4Z	4	3	3,3+	3,3+
TA 1686	PI 603240	-	-	-	-	-	-
TA 1687	PI 603241	4	4	1,2-,3	2=	3	2+,3
TA 1688		4	3+	4	3	3,3+	3
TA 1689		3+	4/;,1,3NZ	4	;,3-	3=	3+
TA 1691		4	3+	4	3	3+	3
TA 1692		4	4	4	3+	2+,3	3
TA 1693	PI 603242	1	;,1	;,1,3-	1=,1	1	2,2-
TA 1694		3+	3,3+	3,3+	3	3+,4	3-
TA 1695	PI 603243	2,2+	2,2+	;,1,2-	;,1-	3,3-	2+
TA 1696		3	2,2+	3+	2	2	1,1+
TA 1699		4	3+	4	3-	3	3
TA 1700		4	3+	4	3=	3+	3=
TA 1703		2	;,2-	4	2-	2++	1,;
TA 1704		4	4	4	3-,3	3+,4	2+,3
TA 1706	PI 603244	-	-	-	-	-	3-
TA 1707	PI 603245	3	2,3	3/2-,3	2	3	2-
TA 1708		4	3+	4	3	3+,4	3
TA 1709		-	-	4	-	-	-
TA 1715		4	4	4	3	3+,4	-
TA 1717		3+	;,1,2-	4	-	1,1-	-
TA 1718		;,1,1+	;,1,2-/;	;,1	1-,1	;,1-	2+
TA 2118		4	4	4	4	3++	3
TA 2119	PI 554324	-	-	-	-	-	3=
TA 2123		-	-	-	3-	-	3
TA 2369	PI 511374	4	4	;,1,2-,3+	2=	3+,4	3
TA 2371		4	3	4	3	3+	3
TA 2373		3+	4	4	3+	;0/3	3
TA 2374		4	4	4	3	3-	3-
TA 2375	PI 603249	4	4	;,1,4Z	2,2++	3+,4	3,3+
TA 2376		1,2	;,1,2-	4	3+,4	2=	3
TA 2377	PI 603250	1,2	2,3	4	2,2+	3,3-	2

APPENDIX I continued

WGGRC accession	GRIN accession	TRTTF	TTKSK	TTTTF	QTHJC	RKQQC	TPMKC
TA 2378	PI 603251	4	;	4	3 LIF	3 LIF	3
TA 2380		3+	4	4	3	3	4
TA 2381	PI 511362	3+	3+	4	3+,4	3+,4	3
TA 2382		3+	2+,3	4	3-	3-	3,3+
TA 2383		4	2,3	4	3+,4	3=	3,3+
TA 2384		3+	4	4	4	3-	3
TA 2385	CIae 2	4	4	4	4	3+,4	3
TA 2387		3+	2,3	4	3=	3	3
TA 2388		3+	4	4	-	3+	3
TA 2389		3+	3	4	3,3+	3	3
TA 2391		3,3+	3+	4	3	3-	3
TA 2393		4	4	4	3	3-	3
TA 2397		4	4	4	3+,4	3	-
TA 2398		4	4	4	4	3+,4	3+
TA 2399		4	4	4	4	3-	-
TA 2401		3+	-	4	3	3+	3
TA 2402		3+	3+	4	-	2+,3	3
TA 2403		3+	4	4	3	3	3
TA 2404		4	4	4	3	3+	-
TA 2405		-	-	-	-	3+	3
TA 2407		4	4	4	3=	3,3-	3-
TA 2409		4	4	4	4	3	3-
TA 2410		4	4	-	3	-	3
TA 2411		4	2,3	4	3	-	-
TA 2412		4	2,3	4	3-	3,3+	3
TA 2413		4	3+	4	2,2+	3+,4	3
TA 2414		4	4	4	3-	3,3+	3-
TA 2415		4	3	-	4	3	3-
TA 2417		4	2,3	4	3=	2++C	3
TA 2418		4	4	4	-	3,3-	3+,4
TA 2419		4	3	4	3-	3,3-	2+,3C
TA 2420		4	4	4	4	3+,4	2+,3C
TA 2421		4	3	4	4	3+,4	3-
TA 2422		4	4	4	3	3,3+	3
TA 2423		4	3,3+	4	4	3+,4	3C
TA 2424		4	3+	4	3+	3,3+	3-
TA 2425		4	4	4	3	3-	-
TA 2426		4	4	4	3	3=	2+C
TA 2427		4	4	4	3,3-	3	3-
TA 2428		4	4	4	3	-	3-
TA 2429		4	3	4	3	2,3=	3,3+
TA 2430		4	4	4	3	3+,4	3,3+
TA 2431		4	4	4	-	3	3-

APPENDIX I continued

WGGRC accession	GRIN accession	TRTTF	TTKSK	TTTTF	QTHJC	RKQQC	TPMKC
TA 2432		4	4	4	3	-	3-
TA 2433		4	4	4	3-	4	3
TA 2434		4	4	4	3+,4	3-	4
TA 2437		3+	4	4	4	3	3
TA 2438		4	4	4	3	2++C	3-
TA 2439		4	4	4	3-	3+,4	3
TA 2440		3+	4	4	4	3,3+	3-
TA 2441		4	4	4	3	3+,4	3
TA 2442		4	3	4	3+	2,2+,3	3+,4
TA 2443	CIae 7	4	3+	4	4	3-	3-
TA 2444		3+	3+	4	3	3,3+	3
TA 2445		3+	4	4	2C	1+,2	3
TA 2447		4	4	4	-	2	3
TA 2454		2,3	2,3-	4	2C	3-	2=
TA 2455		4	4	4	0	-	2=
TA 2457		3	-	;,1,2-	;,1-	3,3+	2+
TA 2460	PI 511377	3+	4	4	4	1+, 3	3,3+
TA 2461	PI 511371	3+	4	4	3	3	3
TA 2467		-	-	-	-	-	-
TA 2468		2,3	2,3	3	2,2-	1+,2	1,1+
TA 2473	CIae 23	-	-	-	-	-	-
TA 2474		;,1	;,1	3	2	1 LIF	1,1+
TA 2477		4	4	4	4	3+,4	3
TA 2478		4	4	4	4	4	4
TA 2479		4	4	4	4	4	3+
TA 2480		;,1N	;,1	3+	-	1+	-
TA 2481		1,2	2-	3+	2	1,2+	1
TA 2482	PI 511364	4	4	4	3	4	2+,3N
TA 2483	PI 511372	1	1,2-	3	0	0	0;
TA 2484		4	;,1	3,3+	2,2-	4	3
TA 2485		4	;,1	1,3+Z	2	4	4
TA 2488		4	3+	4	3	3	3-
TA 2492		4	4	3+	3+,4	3+,4	3
TA 2493		4	4	4	-	3+,4	3+
TA 2494		4	3	4	2	3=	3,3+
TA 2495		1,2	2,3	4	2-	3-	0
TA 2496		4	4/2	4	3	4	4
TA 2498		2+,3	;Y	3+,1Y	2-,2	1,1+	2,2+N
TA 2500		4	4	4	4	3 LIF	3
TA 2502		3	4	4	3	3-	3
TA 2503		4	4	4	3+	3,3+	3+
TA 2504		4	4	4	3+	-	-
TA 2506		-	-	-	4	-	3

APPENDIX I continued

WGGRC accession	GRIN accession	TRTTF	TTKSK	TTTTF	QTHJC	RKQQC	TPMKC
TA 2507		-	4	-	-	3	3
TA 2508		4	4	4	-	-	-
TA 2509		4	4	4	3+	3	3,3+
TA 2511		3+	3,3+	4	4	3+,4	-
TA 2512		4	4	4	3	-	3-
TA 2513		3+	3+	4	3	-	3
TA 2514		3+	4	4	3+	3=	3-
TA 2515		-	4	-	3+	3-	3-
TA 2516		4	3,3+	4	4	3+,4	4
TA 2517		4	3,3+	4	3+,4	3	3+
TA 2518		3,3+	4	4	3	3=,;	3
TA 2519		4	3	4	3-,3	3,3-	3
TA 2520		4	4	4	3	3+,4	3
TA 2521		4	3+	4	3-	3,3+	3
TA 2523		3,3+	2-	2-,3	1	;,1=	1-
TA 2525		1,2,3	4	;,1,2-,3	1-	4	4
TA 2526		3+	3,3+	4	2	3=	-
TA 2527		4	4	4	-	3-	3
TA 2529	PI 603253	4	4	4	2+,3	3+,4	3,3+C
TA 2530	PI 603254	4	4	4	-	2++	3
TA 2531		4	3+	4	3	2+,3	3
TA 2533		4	4	4	2+	3,2-	3
TA 2534		;,3+Z	3+	4	-	2+,3	2+,3 LIF
TA 2535		4	4	-	3+	3	3
TA 2536		4	3+	4	3-	3+	3
TA 2538		4	3,3+	4	3C	2+,3	3
TA 2539		4	3+	-	-	3	-
TA 2540		4	3+	4	3	3	3,3-
TA 2541		4	4	4	3	3,3-	3+,4
TA 2542		4	3+	-	3-	3=	-
TA 2543		4	3,3+	4	3=	3	3,3-
TA 2544		4	4	4	3-	3+,4	3C
TA 2545		4	4	3+	3-	3	3
TA 2546		4	4	4	3+,4	2++,3-	2++
TA 2547		4	4	4	3-	3=	3
TA 2548		4	4	4	-	3=	3=
TA 2549		4	3	3+	2,2-	3=	3
TA 2552		4	4	4	3	3-,3	3
TA 2553		4	3+	4	3	3,3-	3
TA 2554		4	4	4	3	3-	3
TA 2556		4	4	4	3=	3,3-	3=
TA 2557		4	3	4	3,3-	3=	3=,;
TA 2558		4	3	4	-	3=	3-

APPENDIX I continued

WGGRC accession	GRIN accession	TRTTF	TTKSK	TTTTF	QTHJC	RKQQC	TPMKC
TA 2559		4	4	4	4	3,;	3-
TA 2560		4	3+	3+	-	-	-
TA 2561		3+	4	;,1,2-,3	;,1	2++,3	3C
TA 2562		4	4	;,1,2-,3-	1	3+	3+,4
TA 2563		4	4	3,3+	;,1-	3	-
TA 2564		4	;,1	1,2-,3+	1	3+	3,3-+
TA 2567		-	2,2+	4	-	0,;	0;
TA 2568		2+,3+	4	1,2,3	11-	3+	4
TA 2571		4	3+	4	3,3+	3,3+	3
TA 2573		4	3+	4	3,3-	3,3-	3+
TA 2574		4	3,3+	4	4	3	3
TA 2575		3	3	4	3+,4	2++	3
TA 2577		3+	4	4	2+,3	3,3-	3
TA 2578		4	4	1,2-,3	1+	3-,3	4
TA 2579		4	3+	3+	3-	3-,2+	3-
TA 2581		4	3+	4	2+,3	3	3,3-
TA 2582		4	4	4	4	3	3
TA 2583		4	4	4	3	3=,2+	3
TA 2585		4	3+	4	3	3	3+,4
TA 2586		3+	2,2+	4	3-	3	3
TA 2587		4	3	4	3	3+,4	3
TA 10069		4	4	4	3	3	3+,4
TA 10070		4	4	4	3	3,3+	3+,4
TA 10071		4	4	4	3+,4	3=	3
TA 10072		4	4	4	-	-	3
TA 10074		4	4	4	4	3,3+	3
TA 10075		4	4	4	3+	3+,4	3+
TA 10076		4	4	4	3	3,2+,2	3
TA 10077		4	4	4	3+,4	3	4
TA 10078		4	4	4	3+,4	3,;	3
TA 10079		3+	3+	4	3+	3=	3
TA 10080		4	4	4	4	3+,4	3N
TA 10081		1,2	1,2-	3+	1-	1-	0
TA 10082		4	4	4	3+	2++,2	2++N
TA 10083		4	4	4	3	3	3
TA 10084		4	4	4	2+,3	3-	-
TA 10085		2,2+	2+,3	3+	1,2-	2+,3	;,1
TA 10086		1,2	2,3	3+	2N	2,2+	;,1
TA 10087		1	;,2-	;,1C	;,1	3-	1
TA 10088		4	3+	3,3+	3	2+,3	2+,3N
TA 10089		4	4	2-,3	1	3+	3+
TA 10090		4	4	1,2-,3	1-	3+,4	4
TA 10091		4	4	;,1,3	1,1-	2++,3-	3

APPENDIX I continued

WGGRC accession	GRIN accession	TRTTF	TTKSK	TTTTF	QTHJC	RKQQC	TPMKC
TA 10092		1,2	2,2+	;,1,2-,3	1-	3,3-	1,2+
TA 10093		4	4	4	4	3+	3+
TA 10094		4	3,3+	1,3	1	3,3-	2++N
TA 10095		4	4	;,1,3	;,1-	3=,3	3-
TA 10096		4	4	4	3	2++,3,1	2+,3N
TA 10097		4	4	4	4	3+,4	3
TA 10098		3	2,3	4	2N	-	2,2+
TA 10099		3+	2,2+	4	3	2+,3,-1	3
TA 10100		4	2	4	2,2+	2,2-	3
TA 10101		4	3+	;,1,2-	1,1-	2++	3-N
TA 10102		4	3,3+	4	4	3,3-	3,3+
TA 10103		4	4	4	3	3,3+	3-
TA 10104		4	4	4	3	3,2++	3
TA 10105		4	2,3	3+	2 LIF	2++,3-	3-
TA 10106		4	2,2+	4	3+,4	3-,2++	4
TA 10107		4	4	4	3+	3,2++	2++
TA 10108		4	4	4	3-	3	3
TA 10109		4	4	4	-	2+,3-	3
TA 10110		4	3+	4	3+	2++,3-	3
TA 10112		3+	3,3+	4	3+	3+	1,2+N
TA 10113		4	3+	4	1,1+ LIF	3+,4	3,3+
TA 10114		4	4	4	3+,4	3=	3
TA 10115		4	4	4	3	3	3,3+
TA 10116		4	4	4	3+,4	3	3
TA 10118		4	4	1,2,3+	3,4	3	3-C LIF
TA 10119		4	4	4	3	3++	3
TA 10120		4	4	4	3-	3	3
TA 10121		4	4	4	3+	3,3+	3
TA 10122		4	4	4	3	2++	3+,4
TA 10123		4	3,3+	4	2+/4	3	3
TA 10124		1,2	1,1+	1,2-,3-	;,1	3,2++	2,2-
TA 10125		4	4	4	4	3,3+	3
TA 10126		4	4	4	2++	3	3
TA 10127		4	4	3+	2+	3,3-	3
TA 10128		4	3+	4	2++	3-	3- LIF
TA 10129		4	2,2+	4	2	3=	3,3-
TA 10130		4	4	1,2-,3+	1	3++,4	3-
TA 10131		4	4	1,2-,3+	1	3	3-C
TA 10132		4	4	4	4	3+	3
TA 10133		4	4	4	3=	-	-
TA 10134		4	4	-	3	3,3-	3
TA 10135		4	4	4	3	3+	3
TA 10136		4	4	4	3	3	3+

APPENDIX I continued

WGGRC accession	GRIN accession	TRTTF	TTKSK	TTTTF	QTHJC	RKQQC	TPMKC
TA 10137		4	4	4	3	3,2+	4
TA 10138		4	4	4	3-	3	3
TA 10139		4	3+	4	-	3+,4	3
TA 10140		4	4	4	3+	3-	3,3+
TA 10141		4	3+	4	3+	3,3+	3
TA 10142		3	;/;,1+	3,3+	1,1+ LIF	;,3- LIF	1N
TA 10143		4	4	4	3-	3=	3
TA 10144		4	4	4	3-	3,3-	3
TA 10145		4	4	4	3	3=	3
TA 10146		4	4	4	4	3,3+	3
TA 10147		4	;,1N	;,1N	1-,2	0;	0;
TA 10148		4	1,3+	3+N/;,1N	1,2	;/2	1,2++
TA 10149		4	1,3	;,1/3+	1,2	1,;	;,1,2++N
TA 10150		3+	3+	4	1,2	1	;,1,2N
TA 10151		4	3+	3+	1,2+	1,2	;,1,2N
TA 10152		4	1,3+	4	1,2+	1,2	;,1,2+N
TA 10153		3+	1,3+	4	1,2+	1,2	;,1,2+N
TA 10154		4	3+	4	1-,2	1+,2	1-,2
TA 10155		4	4	4	3	2,2+	3-
TA 10156		4	4	4	3	3- LIF	3,3+
TA 10157		4	4	4	3+	3,3-	3
TA 10158		3+	4	4	3+	3-	3
TA 10159		4	4	4	2+,3	2	3
TA 10160		4	4	4	3	3=	3
TA 10161		4	4	4	3	2++	3
TA 10162		4	4	4	-	3	4
TA 10163		4	4	4	3-	2++,3=	3
TA 10164		4	2,3/3+	2,3	3,3+	3,3+	-
TA 10165		4	3+	4	2+,3	3,3+	2+,3N
TA 10166		4	3+	4	3	2++	2+,3N
TA 10167		4	4	4	3	2+,3	2++ LIF
TA 10168		3+	3,3+	3+	2+N	2-,2	2,2+
TA 10169		4	4	3+	2+	2++,3-	2++
TA 10170		4	4	4	3+,4	3+,4	3+
TA 10171		;	;	0;	0	0;	;
TA 10172		4	4	4	3	3	3+,4
TA 10173		4	4	4	3	2,3=	3
TA 10174		4	4	4	3+,4	2++ LIF	3
TA 10175		4	4	4	3	-	3
TA 10176		4	4	4	3-	3,3-	3N LIF
TA 10177		4	4	3	3	;,3=	3N
TA 10178		3+	4	4	3	3,3+	4
TA 10179		;,2=/;/2-	;/;,2=	;/;,1/3-	1	;,1-	;,1-

APPENDIX I continued

WGGRC accession	GRIN accession	TRTTF	TTKSK	TTTTF	QTHJC	RKQQC	TPMKC
TA 10180		4	4	4	-	2++,3-	3
TA 10181		3+	3+	4	1,2	1,1+,2 LIF	1,2+N
TA 10182		4	3+	4	3+	3+,4	3+,4
TA 10183		4	3+	4	3,3+	3+,4	3+,4
TA 10184		3+	4	;,1,2-,3	4	3=	3-
TA 10185		3,3+	3+	4	2C	2++	4
TA 10186		4	4	4	3	3	3- LIF
TA 10187		;	;	;	;,1-	;	0
TA 10188		;	;	;/4	;,1-	;,1=	;,1
TA 10189		4	4	4	3+,4	3-	3
TA 10190		4	4	4	4	3+,4	3N LIF
TA 10191		3+	3,3+	4	3	3+,4	3N
TA 10192		3+	3+	4	3	3+,4	3+,4
TA 10193		3+	3+	4	3+	3+	3+
TA 10194		4	4	2-,3+	2+,3	2+,3	3-
TA 10195		4	3,3+	4	3+	3+,4	3,3+
TA 10196		4	4	4	4	3+	3,3+
TA 10197		4	3+	4	3	3,3-	3-N
TA 10198		4	4	4	4	3+,4	3+
TA 10199		4	3,3+	4	3	3+	3+,4
TA 10200		3+	4	4	4	3+,4	3+,4
TA 10201		3+	;,1,3-	3+	1,2+	;0,1=	;,1,2+
TA 10202		4	4/;,1,3-	3+	1,2	1,1+	;,1,2
TA 10203		3+	;,1,3-	3+	1,2+	1,1+	;,1,2+
TA 10204		3+	;/;,1,3-	1,3+Z	;,1	;,1-2	;,1,2
TA 10205		4	;,1	3+	;,1,2	;,1-	;,1,2
TA 10206		3+	;,1	1,3-Z	;,1	;,1=	;,1=
TA 10208		3+	;,1,3	1,3Z	1,2	1-,1+	1,2
TA 10210		3+	3+	3+	-	3	3N
TA 10211		4	3+	4	3	3+,4	3+
TA 10212		4	4	4	3	3,3+	3+,4
TA 10213		4	4	4	3-	3+,4	4
TA 10293		4	4	4	3	3+	4
TA 10294		4	3	4	3	3+,4	4
TA 10295		4	3,3+	4	3+	3+,4	3-
TA 10297		3+	3	4	3	3,3+	3
TA 10298		4	4	4	3	3+,4	4
TA 10299		4	3	4	3	;,3-	-
TA 10300		-	3	-	3	3	4
TA 10301		4	3	4	-	-	3
TA 10302		4	2,3	4	3-	3+	3
TA 10303		4	3	4	3	3	3
TA 10304		4	4	4	3-	3=,3+	3

APPENDIX I continued

WGGRC accession	GRIN accession	TRTTF	TTKSK	TTTTF	QTHJC	RKQQC	TPMKC
TA 10305		4	4	4	2C	3,3+	3-
TA 10306		4	4	4	3+	;,3 LIF	3N
TA 10308		4	4	4	3	3+	3+,4
TA 10309		4	4	4	2C	3-	3
TA 10310		4	4/2,3	4	3	3+	3,4
TA 10311		3+	4	4	3-	3+	3
TA 10312		3+	4	4	3	3	3-
TA 10313		3+	3	3+	3	;,3 LIF	4
TA 10314		4	4	4	3+	3+,4	3+
TA 10316		3+	2,3	3+	-	3-	3
TA 10317		3+	2,3	3+	3	3	3
TA 10318		3+	2,3	3+	3	3-/4	3
TA 10319		3+	3+	3+	3-	3+,4	3
TA 10320		4	4	4	4	3	3+,4
TA 10322		4	3+	3+	3	-	3
TA 10323		4	4	4	4	3+,4	3,3+
TA 10324		4	4	4	2+	3+,4	3
TA 10325		4	4	4	2++	3+	3
TA 10326		3+	3	3+	3,3-	3	2,2-C
TA 10327		3+	4	4	4	3+	4
TA 10328		4	3+	4	3	3-	4
TA 10329		4	4	4	3+	3+,4	4
TA 10330		4	4	4	3	2,2+	3,3+
TA 10331		4	4	4	3+	2/3	3,3+
TA 10417		4	4	4	4	3+,4	3
	CIae 2	-	-	-	3	3+,4	4
	CIae 5	3	3	3	3	2+,3	-
	CIae 15	2+,3	1,2-;	4	3+,4	2-	3
	CIae 19	-	-	-	-	-	-
	CIae 25	2	2-2Z	3+	2N	3=	;,1,1-
	CIae 26	3+	3	4	4	3+	4
	CIae 30	3+	3	1,2-	1	-	2+
	CIae 50	4	3+	3+	2+C	3	3
	CIae 51	3+	3+	3+	3	2+,3	-
	CIae 68	4	2,3Z	4	3-	3+,4	4
	CIae 71	4	3+	3+	3-	-	4
	CIae 72	3-	2-2	3+	-	-	-
	PI 210987	3+	2,2+	3+	3,3+	3+	3+,4
	PI 276975	3+	3-	3	4	3+	3+,4
	PI 276980	3+	3	2-	;,1	3+,4	4
	PI 330489	4	3-	3+	3C	3+,4	4
	PI 369627	2+,3	;,2/2+	1,2-,2	;,1-	2/2+	1,2C
	PI 431603	;,1,1+	;,1,2-	1,;,2-	-	-	-

APPENDIX I continued

WGGRC accession	GRIN accession	TRTTF	TTKSK	TTTTF	QTHJC	RKQQC	TPMKC
	PI 452130	3+	3-	3+	3	0;/0;,1-/0;,1	3
	PI 452131	4	3-/3	4	4	3,3+	4
	PI 499262	3	3	3+	4	3+,4	4
	PI 499265	3+	3-	3+	3-	-	3
	PI 508261	3+	3	3+	3+	3+,4	3+,4
	PI 508263	3+	3	3+	3	3	;0/3
	PI 508264	3+	3	3+	3	2+,3	3- LIF
	PI 554311	3	3	3+	3	3+,4	3+
	PI 554313	3	3	3+	3+	3+,4	3
	PI 554315	3/3+	3	3+	3+	3,3+	3
	PI 554316	3+	4	3+	-	-	-
	PI 554318	3+	3	3+	3+	3+,4	3
	PI 554319	3+	2+	3+/3	3,3-	3+,4	3
	PI 554320	2-	2,2+Z	3+/4	3-	3	-
	PI 554321	3+	3	3	3-	3+,4	-
	PI 554322	-	-	-	-	-	-
	PI 554323	4	3+	3+	3+	3+	3
	PI 560534	3+	3-	3	4	3+ LIF	3
	PI 560535	3+	3-	3,3+	4	3-	3
	PI 560536	3+	3	3+	4	3,3+	3
	PI 560538	3+	3-	3,3+	3	3	4
	PI 560754	3+	3-	3,3+	3+,4	3+	4
	PI 560755	3+	3-/3	4	3+,4	3-	3+,4
	PI 574468	3	3-	3,3+	4	3- LIF	3
	PI 574469	2-/3+	3-	4	2+,3	-	2+,3N
	PI 603249	0/3+ LIF	3	2+,3/2-/3	;,1,2	3-	3-

APPENDIX II: *Triticum urartu* and *Triticum monococcum* screening data

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post. [a]
CItr 17664	*T. urartu*	Lebanon	4	2-	3+	4	4	
CItr 17666	*T. urartu*	Lebanon	4	2-	3+	4	3	
CItr 17667	*T. urartu*	Turkey	4	2-	4	4	4	
CItr 17668	*T. urartu*	Armenia	4	2	4	4	4	
PI 427328	*T. urartu*	Iraq	-	;2-	3+	-	-	
PI 428180	*T. urartu*	Armenia	4	2	4	4	4	
PI 428181	*T. urartu*	Armenia	4	2-/2	4	4	4	
PI 428182	*T. urartu*	Armenia	4	2-	4	4	4	
PI 428183	*T. urartu*	Armenia	4	2-	4	4	4	
PI 428184	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428185	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428186	*T. urartu*	Turkey	4	4	4	4	4	
PI 428187	*T. urartu*	Turkey	-	-	4	-	-	
PI 428188	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428189	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428190	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428191	*T. urartu*	Turkey	4	4	4	4	4	
PI 428192	*T. urartu*	Turkey	-	-	3+	4	-	
PI 428193	*T. urartu*	Turkey	4	2	4	4	4	
PI 428194	*T. urartu*	Turkey	4	2-	4	-	-	
PI 428195	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428196	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428197	*T. urartu*	Turkey	4	2	4	4	4	
PI 428198	*T. urartu*	Turkey	4	2	4	4	4	
PI 428199	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428200	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428201	*T. urartu*	Turkey	4	4	4	4	4	
PI 428202	*T. urartu*	Turkey	4	2-	4	4	-	
PI 428203	*T. urartu*	Turkey	4	2-	3+	4	4	
PI 428204	*T. urartu*	Turkey	4	4	3+	4	4	
PI 428205	*T. urartu*	Turkey	4	2	4	4	4	
PI 428206	*T. urartu*	Turkey	4	2/4	4	4	4	
PI 428207	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428208	*T. urartu*	Turkey	4	2-	3+	4	4	
PI 428209	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428210	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428211	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428212	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428213	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428214	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428215	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428216	*T. urartu*	Turkey	4	2	4	4	4	
PI 428217	*T. urartu*	Turkey	4	-	3+	-	3+	
PI 428218	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428219	*T. urartu*	Turkey	4	2	4	4	4	
PI 428220	*T. urartu*	Turkey	4	2-	3+	4	4	
PI 428221	*T. urartu*	Turkey	4	2-	4	4	4	

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 428222	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428223	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428224	*T. urartu*	Turkey	4	2	4	4	-	
PI 428225	*T. urartu*	Turkey	-	-	4	-	-	
PI 428226	*T. urartu*	Turkey	4	2-	4	-	-	
PI 428227	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428228	*T. urartu*	Turkey	-	2-	4	4	-	
PI 428229	*T. urartu*	Turkey	4	2	4	4	4	
PI 428230	*T. urartu*	Turkey	4	2	4	4	4	
PI 428231	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428232	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428233	*T. urartu*	Turkey	4	2	4	4	4	
PI 428234	*T. urartu*	Turkey	4	-	4	4	4	
PI 428235	*T. urartu*	Turkey	-	2-	3+	4	4	
PI 428236	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428237	*T. urartu*	Turkey	4	2	4	4	4	
PI 428238	*T. urartu*	Turkey	4	2	4	4	4	
PI 428239	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428240	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428241	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428242	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428243	*T. urartu*	Turkey	4	2	4	-	4	
PI 428244	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428245	*T. urartu*	Turkey	4	2	4	4	4	
PI 428246	*T. urartu*	Turkey	-	-	4	-	4	
PI 428247	*T. urartu*	Turkey	4	-	4	4	4	
PI 428248	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428249	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428250	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428251	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428252	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428253	*T. urartu*	Iraq	4	4	4	-	-	
PI 428254	*T. urartu*	Turkey	4	2-	4	4	4	
PI 428255	*T. urartu*	Turkey	-	2-	4	-	4	
PI 428256	*T. urartu*	Turkey	4	2-	-	4	-	
PI 428257	*T. urartu*	Armenia	4	2-	4	4	4	
PI 428258	*T. urartu*	Armenia	4	2	4	4	4	
PI 428259	*T. urartu*	Armenia	4	2-	4	4	4	
PI 428260	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428261	*T. urartu*	Lebanon	4	2-	4	4	3	
PI 428262	*T. urartu*	Lebanon	4	2-	4	4	3	
PI 428263	*T. urartu*	Lebanon	4	2-	4	4	3	
PI 428264	*T. urartu*	Lebanon	4	2-	4	4	3	
PI 428265	*T. urartu*	Lebanon	4	2-	4	4	3	
PI 428266	*T. urartu*	Lebanon	4	2-	4	4	3	
PI 428267	*T. urartu*	Lebanon	4	2-	4	4	3	
PI 428268	*T. urartu*	Lebanon	4	2-	4	4	3	

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 428269	*T. urartu*	Lebanon	4	2	4	4	4	
PI 428270	*T. urartu*	Lebanon	4	2-	4	4	3	
PI 428271	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428272	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428273	*T. urartu*	Lebanon	4	2-	4	4	;3	
PI 428274	*T. urartu*	Lebanon	4	2-	4	4	;3	
PI 428275	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428276	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428277	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428278	*T. urartu*	Lebanon	4	2-	4	4	;3	
PI 428279	*T. urartu*	Lebanon	4	2-	4	4	;3	
PI 428280	*T. urartu*	Lebanon	4	2-	4	4	;3	
PI 428281	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428282	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428283	*T. urartu*	Lebanon	4	2	4	4	4	
PI 428284	*T. urartu*	Lebanon	4	2-	4	4	3	
PI 428285	*T. urartu*	Lebanon	4	2-	4	4	13	
PI 428286	*T. urartu*	Lebanon	4	2-	4	4	13	
PI 428287	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428288	*T. urartu*	Lebanon	4	2-	4	4	3	
PI 428289	*T. urartu*	Lebanon	-	2-	4	-	;3	
PI 428290	*T. urartu*	Lebanon	-	2-	4	4	;13-	
PI 428291	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428292	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428293	*T. urartu*	Lebanon	4	2	4	4	;13-	
PI 428294	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428295	*T. urartu*	Lebanon	4	2-	4	4	;13-	
PI 428296	*T. urartu*	Lebanon	4	2-/4	4	4	;13/3	
PI 428297	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428298	*T. urartu*	Lebanon	-	-	4	4	;13-	
PI 428299	*T. urartu*	Lebanon	4	2-	4	4	;13-	
PI 428300	*T. urartu*	Lebanon	4	2-	4	4	;13-	
PI 428301	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428302	*T. urartu*	Lebanon	4	2-	4	4	;3	
PI 428303	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428304	*T. urartu*	Lebanon	4	2-	4	4	;13-	
PI 428305	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428306	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428307	*T. urartu*	Lebanon	4	-	-	4	;13	
PI 428308	*T. urartu*	Lebanon	-	-	4	-	-	
PI 428309	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428310	*T. urartu*	Lebanon	4	2-	4	-	-	
PI 428311	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428312	*T. urartu*	Lebanon	4	2-	4	4	13-	
PI 428313	*T. urartu*	Lebanon	4	2-	4	4	;13-	
PI 428314	*T. urartu*	Lebanon	4	2-	4	4	;13-	
PI 428315	*T. urartu*	Lebanon	4	-	4	4	-	

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 428316	*T. urartu*	Iran	4	4	4	4	4	
PI 428318	*T. urartu*	Turkey	4	2-	4	4	3	
PI 428320	*T. urartu*	Lebanon	4	2-	4	4	;1	
PI 428321	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428322	*T. urartu*	Lebanon	4	2-	4	4	;13-	
PI 428323	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428324	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428325	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428326	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428327	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428328	*T. urartu*	Lebanon	4	2-	4	3	4	
PI 428329	*T. urartu*	Lebanon	4	-	-	-	-	
PI 428330	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428331	*T. urartu*	Lebanon	-	-	4	4	-	
PI 428332	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428333	*T. urartu*	Lebanon	4	2-	4	4	;3	
PI 428334	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 428335	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 428336	*T. urartu*	Lebanon	4	2-	4	4	;1	
PI 428338	*T. urartu*	Lebanon	4	2-	-	-	;13-	
PI 428339	*T. urartu*	Lebanon	4	2-	4	22+	2-2	
PI 428340	*T. urartu*	Lebanon	4	2-	4	-	;13-	
PI 428341	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 487265	*T. urartu*	Syria	4	2-	4	4	4	
PI 487266	*T. urartu*	Syria	4	2-	4	4	4	
PI 487267	*T. urartu*	Syria	4	2-	4	4	4	
PI 487268	*T. urartu*	Syria	4	2-	4	4	4	
PI 487269	*T. urartu*	Syria	4	2-	4	4	4	
PI 487270	*T. urartu*	Syria	4	4	4	4	4	
PI 487271	*T. urartu*	Syria	4	-	4	4	4	
PI 487272	*T. urartu*	Syria	4	2-	4	4	4	
PI 503319	*T. urartu*	Turkey	4	4/2	4	2+3	4/;1	
PI 538724	*T. urartu*	Turkey	4	2-	3+	2+3	1	
PI 538725	*T. urartu*	Turkey	4	2-	4	4	4	
PI 538726	*T. urartu*	Turkey	-	2-	4	4	-	
PI 538727	*T. urartu*	Turkey	4	2-	4	4	4	
PI 538728	*T. urartu*	Turkey	4	-	4	4	4	
PI 538729	*T. urartu*	Turkey	4	2-	4	4	4	
PI 538730	*T. urartu*	Turkey	4	2-	4	4	4	
PI 538731	*T. urartu*	Turkey	4	2-	4	4	4	
PI 538732	*T. urartu*	Turkey	4	2-	4	4	4	
PI 538733	*T. urartu*	Turkey	4	2-	3	2+3/4	4/12-	
PI 538734	*T. urartu*	Lebanon	4	2-	4	4	;13-	
PI 538735	*T. urartu*	Lebanon	4	2-	4	4	;13-	
PI 538736	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 538737	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 538738	*T. urartu*	Lebanon	4	2-	4	4	;13-	

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 538739	*T. urartu*	Lebanon	4	2-	4	4	;3	
PI 538740	*T. urartu*	Lebanon	-	2-	4	-	-	
PI 538741	*T. urartu*	Lebanon	-	-	-	-	-	
PI 538742	*T. urartu*	Lebanon	4	2-	4	4	;3	
PI 538743	*T. urartu*	Lebanon	4	2-	4	4	;13	
PI 538744	*T. urartu*	Lebanon	-	-	4	4	13	
PI 538745	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 538746	*T. urartu*	Lebanon	4	2-	4	-	;13-	
PI 538747	*T. urartu*	Lebanon	4	2-	4	4	-	
PI 538748	*T. urartu*	Lebanon	4	-	4	4	-	
PI 538749	*T. urartu*	Lebanon	4	2-	4	4	-	
PI 538750	*T. urartu*	Lebanon	-	-	-	-	-	
PI 538751	*T. urartu*	Lebanon	4	2-	4	4	4	
PI 554597	*T. urartu*	Turkey	4	4/2	4	4	4	
PI 554598	*T. urartu*	Turkey	4	4/2-	4	4	4	
PI 554599	*T. urartu*	Turkey	4	2-	4	4	4	
PI 554600	*T. urartu*	Turkey	4	2-/4	4	4	4	
CI 17665	*T. m. a.* [b]	Iran	3	1;	3	4	1	*Sr21*
CI 17670	*T. m. a.*	Lebanon	3	22+Z	3	4	1	*Sr21*
CI 17671	*T. m. a.*	Turkey	3	1/12Z	4	22+	;1	*Sr21* +
CI 17672	*T. m. a.*	Azerbaijan	3/3+	2+3Z	4	4	1	*Sr21*
CI 17673	*T. m. a.*	Iraq	3+	1/3-	3+	22+	1	*Sr21* +
CI 17674	*T. m. a.*	Iran	3+	2++	3+	22+	1	*Sr21* +
CI 17741	*T. m. a.*	United States	3/3+	2++	4	4	;1	*Sr21*
PI 245726	*T. m. a.*	Turkey	3	-	4	4	4	Sus. [c]
PI 272519	*T. m. a.*	Hungary	2-	1	2	-	-	*Sr22*
PI 272520	*T. m. a.*	Hungary	2-	;2-	2	1	;1	*Sr22*
PI 272556	*T. m. a.*	Hungary	3+	4	3	4	4	Sus.
PI 277121	*T. m. a.*	Germany	4	2+3Z	4	4	;1	*Sr21*
PI 306527	*T. m. a.*	Romania	4	3	3+	4	4	Sus.
PI 306532	*T. m. a.*	Romania	4	4	3+	4	4	Sus.
PI 330527	*T. m. a.*	United Kingdom	4	4	3+	-	4/;1	Het
PI 330528	*T. m. a.*	United Kingdom	12-;	1;	12-;	;1	;1	*Sr22*
PI 352266	*T. m. a.*	Asia Minor	12-	1;	2-	;1	;1	*Sr22*
PI 352267	*T. m. a.*	Asia Minor	12-	1;	2-	;1	;1	*Sr22*
PI 352269	*T. m. a.*	Germany	2-	1;	2-	;1	;1	*Sr22*
PI 352270	*T. m. a.*	Germany	4	2+3Z	4	4	1	*Sr21*
PI 352271	*T. m. a.*	Asia Minor	2-/2	2-	2	2-	;1	*Sr22*
PI 352272	*T. m. a.*	Balkans	12-	1;/4	12-	;1	;1	*Sr22* *Het*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 352273	*T. m. a.*	Asia Minor	4	12Z	4	4	1	*Sr21*
PI 352274	*T. m. a.*	Asia Minor	4	4	4	4	4	Sus.
PI 352276	*T. m. a.*	Germany	3+	12Z/22+ Z	4	4	;1	*Sr21*
PI 352277	*T. m. a.*	Asia Minor	3	22+Z	3+	4/22+	;1	*Sr21+ Het*
PI 352501	*T. m. a.*	Asia Minor	3	2+3Z/22 +Z	3+	4	1+3-	*Sr21*
PI 352502	*T. m. a.*	Asia Minor	3+	1	3	;1	;1	*Sr21+*
PI 352503	*T. m. a.*	Iran	3+	22+Z	4	3	;1	*Sr21*
PI 352504	*T. m. a.*	Germany	2	2-	2	;2-	;1	*Sr22*
PI 352505	*T. m. a.*	Switzerland	2	;1	2-2	;1	;1	*Sr22*
PI 355453	*T. m. a.*	Asia Minor	4	2	3	4	1	*Sr21*
PI 374574	*T. m. a.*	Yugoslavia	1;	;1	1;	;1	;1	*Sr22*
PI 374575	*T. m. a.*	Yugoslavia	1;	;1	2-	;1	;1	*Sr22 Sr21*
PI 381063	*T. m. a.*	Iran	3+	12Z	3+	4	4/1+	*Het*
PI 401410	*T. m. a.*	Iran	3+	4	3+	4	4/;1	Het
PI 401411	*T. m. a.*	Iran	3+	4	3+	4	4	Sus.
PI 401412	*T. m. a.*	Iran	3	3	3	22+	3+	-
PI 401413	*T. m. a.*	Iran	4	1/2+3Z	3	22+	1+	*Sr21+*
PI 401414	*T. m. a.*	Iran	4	22+Z	4	4	1	*Sr21 Sr21+*
PI 401416	*T. m. a.*	Iran	3+	2+	3+	4/2 ;1LIF/2	1	*Het*
PI 418580	*T. m. a.*	Azerbaijan	4	3+	4	+3	4/;1	-
PI 427405	*T. m. a.*	Iraq	3+	2+3Z	3	22+	1	*Sr21+*
PI 427443	*T. m. a.*	Turkey	1;	1;	4	-	-	-
PI 427444	*T. m. a.*	Turkey	3+	22+Z	3+	22+	1	*Sr21+*
PI 427445	*T. m. a.*	Turkey	3+	22+Z	3+	;/2	1	*Sr21+ Sr22*
PI 427446	*T. m. a.*	Turkey	2-/3+	2-/3	2-	2-/2	;1	*Het*
PI 427447	*T. m. a.*	United Kingdom	2-	12-Z	2-	;1	;1	*Sr22*
PI 427448	*T. m. a.*	Turkey	4	2+3Z	3+	22+	1	*Sr21+ Sr22*
PI 427449	*T. m. a.*	Turkey	2/3	1/12Z	2+2	2/4	;1	*Het*
PI 427450	*T. m. a.*	Turkey	3+	3-	3+	22+	1+	*Sr21*
PI 427451	*T. m. a.*	Turkey	3+	3	3	2	1	-
PI 427452	*T. m. a.*	Turkey	4	12Z	3+	3	1	*Sr21*
PI 427453	*T. m. a.*	Turkey	4	22+Z	3+	3+	1	*Sr21*
PI 427454	*T. m. a.*	Turkey	3+	3	3+	22+	1+3-	*Sr21+*
PI 427455	*T. m. a.*	Turkey	3+	2+3Z	4	3+	1	*Sr21*
PI 427456	*T. m. a.*	Turkey	-	2	3	-	-	-
PI 427457	*T. m. a.*	Turkey	3	3	3	2	1+3-	*Sr21+*
PI 427458	*T. m. a.*	Turkey	4	22+Z	3	4	1	*Sr21 Sr21+*
PI 427459	*T. m. a.*	Turkey	3+	12-Z/3	3	;1/22+	2-/4	*Het*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427461	*T. m. a.*	United Kingdom	4	4	4	4	4	Sus.
PI 427462	*T. m. a.*	United Kingdom	1+	12-Z	2-2	;1	;1	*Sr22*
PI 427463	*T. m. a.*	Azerbaijan	2-	1N	2-	1;	;1	*Sr22*
PI 427464	*T. m. a.*	Azerbaijan	4	2+3Z	3	22+	;1	*Sr21+*
PI 427465	*T. m. a.*	Armenia	4	2+3Z	4	3+	2	*Sr21*
PI 427467	*T. m. a.*	Azerbaijan	3+	2+3Z	4	4	2	*Sr21*
PI 427468	*T. m. a.*	Azerbaijan	3+	2+3Z	4	4	1	*Sr21*
PI 427469	*T. m. a.*	Azerbaijan	4	2+3Z	3+	2-/22+	1	*Sr21+*
PI 427470	*T. m. a.*	Turkey	3+	1	3+	2	;1	*Sr21+*
PI 427471	*T. m. a.*	Turkey	3+	-	3+	-	-	-
PI 427472	*T. m. a.*	Turkey	4	1	4	22+	;1	*Sr21+*
PI 427473	*T. m. a.*	Turkey	4	1	4	22+/4	;1	*Sr21+ Het*
PI 427474	*T. m. a.*	Turkey	3+	12Z	3	22+	;1	*Sr21+*
PI 427475	*T. m. a.*	Turkey	3+	12-Z	3	22+	-	*Sr21*
PI 427476	*T. m. a.*	Turkey	4	1	4	22+	;1	*Sr21+*
PI 427477	*T. m. a.*	Turkey	4	12-Z	3+	22+	;1	*Sr21+*
PI 427478	*T. m. a.*	Turkey	3+	1/12Z	3	22+	;1	*Sr21+*
PI 427479	*T. m. a.*	Turkey	3+	3	4	4	11+	*Sr21 Sr21+*
PI 427480	*T. m. a.*	Turkey	4	1/12+Z	3	22+/3+	11+	*Het*
PI 427481	*T. m. a.*	Turkey	4	1/2+Z	3	22+	;1	*Sr21+*
PI 427482	*T. m. a.*	Turkey	4	12Z	3-	-	1	*Sr21*
PI 427483	*T. m. a.*	Turkey	4	2	4	4	4	-
PI 427484	*T. m. a.*	Turkey	4	2/2+Z	4	3+	;1	*Sr21*
PI 427485	*T. m. a.*	Turkey	4	3	3	-	-	-
PI 427486	*T. m. a.*	Turkey	4	2+/1	3	-	-	*Sr21*
PI 427487	*T. m. a.*	Turkey	4	1	3	-	-	*Sr21*
PI 427488	*T. m. a.*	Turkey	4	22+Z	3+	2	22+	*Sr21+*
PI 427489	*T. m. a.*	Turkey	4	12+Z	4	-	2	*Sr21*
PI 427490	*T. m. a.*	Turkey	4	12Z	3+	22+	1	*Sr21+*
PI 427491	*T. m. a.*	Turkey	4	2+/12Z	4	22+	-	*Sr21+*
PI 427492	*T. m. a.*	Turkey	4	22+Z	4	22+/2+3	11+	*Sr21+*
PI 427493	*T. m. a.*	Turkey	4	2	3+	22+	12	*Sr21+*
PI 427494	*T. m. a.*	Turkey	3+	2+	3+	22+	12	*Sr21+*
PI 427495	*T. m. a.*	Turkey	4	2+3Z	4	3+	11+	*Sr21*
PI 427496	*T. m. a.*	Turkey	4	22+Z	3	22+	1	*Sr21+*
PI 427497	*T. m. a.*	Turkey	4	22+Z	4	4	1	*Sr21*
PI 427498	*T. m. a.*	Turkey	4	3	3	22+	22+	*Sr21+*
PI 427499	*T. m. a.*	Turkey	4	23-Z	3	-	-	*Sr21*
PI 427500	*T. m. a.*	Turkey	4	123Z	4	22+	1	*Sr21*
PI 427501	*T. m. a.*	Turkey	-	3	-	-	-	-
PI 427502	*T. m. a.*	Turkey	4	123+Z	3	22+	;1	*Sr21+*
PI 427503	*T. m. a.*	Turkey	3+	123Z	3	22+	;1	*Sr21+*
PI 427504	*T. m. a.*	Turkey	3+	123Z	4	2+3	;1	*Sr21+*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427505	*T. m. a.*	Turkey	3+	-	3	22+	1	*Sr21+*
PI 427506	*T. m. a.*	Turkey	4	22+Z	3	22+	1	*Sr21+*
PI 427507	*T. m. a.*	Turkey	3+	3	3	22+	1	*Sr21+*
PI 427508	*T. m. a.*	Turkey	4	123-Z	4	3+	1	*Sr21*
PI 427509	*T. m. a.*	Turkey	3+	12+Z	3	2+3	;1	*Sr21+*
PI 427510	*T. m. a.*	Turkey	3+	3	3	22+	22+	*Sr21+*
PI 427511	*T. m. a.*	Turkey	3+	1;	3	22+/3+	1	*Sr21+* *Het*
PI 427512	*T. m. a.*	Turkey	3	123Z	4	22+	1	*Sr21+*
PI 427513	*T. m. a.*	Turkey	3+	2+3Z	4	22+	12-	*Sr21+*
PI 427514	*T. m. a.*	Turkey	3+	12-	3	22+	1	*Sr21+*
PI 427515	*T. m. a.*	Turkey	3+	12+Z	3	22+	1	*Sr21+*
PI 427516	*T. m. a.*	Turkey	3+	123Z	4	4	4	-
PI 427517	*T. m. a.*	Turkey	3+	123-Z	4	22+	;1	*Sr21*
PI 427518	*T. m. a.*	Turkey	3+	123Z	3/4	2/22+	;1	*Sr21+*
PI 427519	*T. m. a.*	Turkey	3+	2+3Z	3	22+	22+	*Sr21+*
PI 427520	*T. m. a.*	Turkey	3+	12+Z/3	3+	22+	;1	*Sr21+*
PI 427521	*T. m. a.*	Turkey	3	12+Z	3	22+	;1	*Sr21+*
PI 427522	*T. m. a.*	Turkey	3	12+Z	3	22+	;1	*Sr21+*
PI 427523	*T. m. a.*	Turkey	3+	12+Z/3	3	-	1	*Sr21*
PI 427524	*T. m. a.*	Turkey	3+	2+3Z	3+	22+	;1	*Sr21+*
PI 427525	*T. m. a.*	Turkey	3+	2+3Z	3	22+	1	*Sr21+*
PI 427526	*T. m. a.*	Turkey	4	2+3Z	4	22+	;1	*Sr21+*
PI 427527	*T. m. a.*	Turkey	4	12+Z	3+	4	;1	*Sr21*
PI 427528	*T. m. a.*	Turkey	3+	1;	3	22+	-	*Sr21+* *Sr22*
PI 427529	*T. m. a.*	Turkey	3/1	1;/2+	3/2/2-	22+	1	*Het*
PI 427530	*T. m. a.*	Turkey	3	1;/2	3	-	2	*Sr21*
PI 427531	*T. m. a.*	Turkey	3	2+3Z	3	22+	1	*Sr21+*
PI 427532	*T. m. a.*	Turkey	3+	2	3	1+2	;1	*Sr21+*
PI 427533	*T. m. a.*	Turkey	3+	2	3	22+	-	*Sr21+*
PI 427534	*T. m. a.*	Turkey	4	12-Z	3	2+3-	;1	*Sr21+*
PI 427535	*T. m. a.*	Turkey	3+	3/12+Z	3	22+	1	*Sr21+*
PI 427536	*T. m. a.*	Turkey	3+	2+3Z/2	3	2	1	*Sr21+*
PI 427537	*T. m. a.*	Turkey	3/3+	1;	3	22+	;1	*Sr21+*
PI 427538	*T. m. a.*	Turkey	3+	2+3Z	3	22+	12-	*Sr21+*
PI 427539	*T. m. a.*	Turkey	4	2+3Z	3	2+3	12-	*Sr21+*
PI 427540	*T. m. a.*	Turkey	4	2+3Z	3	3+	1	*Sr21*
PI 427541	*T. m. a.*	Turkey	3+	12+Z	3	3+	1	*Sr21*
PI 427542	*T. m. a.*	Turkey	3+	23Z	3	3+	1	*Sr21*
PI 427543	*T. m. a.*	Turkey	3+	23Z	3	3+	12-	*Sr21*
PI 427544	*T. m. a.*	Turkey	4	33+	4	4	;1	-
PI 427545	*T. m. a.*	Turkey	4	2/2+	4	4	;1	*Sr21*
PI 427546	*T. m. a.*	Turkey	4	23Z-	3+	4	;1	*Sr21*
PI 427547	*T. m. a.*	Turkey	4	-	4	4	-	-
PI 427548	*T. m. a.*	Turkey	4	3+	4	-	-	-
PI 427549	*T. m. a.*	Turkey	4	3+	3+	3+	;1	-

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427550	*T. m. a.*	Turkey	3+	3+	4	3+	;1	-
PI 427551	*T. m. a.*	Turkey	4	23Z	4/3	2+3	;1	*Sr21*+
PI 427552	*T. m. a.*	Turkey	3+	2+Z	4	-	-	*Sr21*
PI 427553	*T. m. a.*	Turkey	3	2+Z/3	4	4	;1	*Sr21*
PI 427554	*T. m. a.*	Turkey	-	-	3	-	-	-
PI 427555	*T. m. a.*	Turkey	4	2	3	4	;1	*Sr21*
PI 427556	*T. m. a.*	Turkey	4	12+Z	4	4	;	*Sr21*
PI 427557	*T. m. a.*	Turkey	3	2	4	4	4	-
PI 427558	*T. m. a.*	Turkey	3	12Z	3	22+	-	*Sr21*+
PI 427559	*T. m. a.*	Turkey	3	3	3	-	3	Sus.
PI 427560	*T. m. a.*	Turkey	3+	3+/1;	3	3	3	Het
PI 427561	*T. m. a.*	Turkey	3+	3	3	3+	2/3/3+	Het
PI 427562	*T. m. a.*	Turkey	4	3+	3	3+	3	Sus.
PI 427563	*T. m. a.*	Turkey	3+	3+	3	3+	3+	Sus.
PI 427564	*T. m. a.*	Turkey	4	3+	4	4	23+Z	-
PI 427565	*T. m. a.*	Turkey	3	2+3Z	3	4/3	2-	*Sr21*
PI 427566	*T. m. a.*	Turkey	3	3	3	3+	3	Sus.
PI 427567	*T. m. a.*	Turkey	3+	1	3/2+	3+	;1	*Sr21*+
PI 427568	*T. m. a.*	Turkey	3+	23Z	4	-	;1	*Sr21*
PI 427569	*T. m. a.*	Turkey	3+	3	4	2+3	12	*Sr21*+
PI 427570	*T. m. a.*	Turkey	3+	123Z	4	22+	;1	*Sr21*+
PI 427571	*T. m. a.*	Turkey	3+	-	4	-	;1	*Sr21*
PI 427572	*T. m. a.*	Turkey	4	12Z/23Z	4	22+	;1	*Sr21*+
PI 427573	*T. m. a.*	Turkey	4	2+3Z	4	2+3	;1	*Sr21*+
PI 427574	*T. m. a.*	Turkey	3+	2+3Z	4	3+	-	*Sr21*
PI 427575	*T. m. a.*	Turkey	3	3	4	-	;1	*Sr21*
PI 427576	*T. m. a.*	Turkey	4	-	4	-	-	-
PI 427577	*T. m. a.*	Turkey	3+	2+3Z	4	4	;1	*Sr21*
PI 427578	*T. m. a.*	Turkey	4	23Z/3+	4	3+	;1	*Sr21*
PI 427579	*T. m. a.*	Turkey	4	2	4	2+3	;1	*Sr21*+
PI 427580	*T. m. a.*	Turkey	4	123Z	4	4	;1	*Sr21*
PI 427581	*T. m. a.*	Turkey	3+	123Z	4	2+3	;1	*Sr21*+
PI 427582	*T. m. a.*	Turkey	3+	12+Z	4	2+3	;1	*Sr21*+
PI 427583	*T. m. a.*	Turkey	3	12+Z	4	22+	;1	*Sr21*+
PI 427584	*T. m. a.*	Turkey	3+	2-	4	-	;1	*Sr21*
PI 427585	*T. m. a.*	Turkey	4	123Z	4	4	;1	*Sr21*
PI 427586	*T. m. a.*	Turkey	3+	1+	4	3+	;1	*Sr21*
PI 427587	*T. m. a.*	Turkey	3+	123Z	4	4	;1	*Sr21*
PI 427588	*T. m. a.*	Turkey	4	23Z	4	3+	;1	*Sr21*
PI 427589	*T. m. a.*	Turkey	4	23Z	4	3+	;1	*Sr21*
PI 427590	*T. m. a.*	Turkey	4	123Z	4	2+3	;1	*Sr21*+
PI 427591	*T. m. a.*	Turkey	3+	2+3Z	3-	3+	;1	*Sr21*
PI 427592	*T. m. a.*	Turkey	4	12+Z	3	4	;1	*Sr21*
PI 427593	*T. m. a.*	Turkey	3+	123Z	3	4	;1	*Sr21*
PI 427594	*T. m. a.*	Turkey	4	123Z	3	3+	;1	*Sr21*
PI 427595	*T. m. a.*	Turkey	4	2+3Z	3	3+	;1	*Sr21*
PI 427596	*T. m. a.*	Turkey	4	12+Z	3	4	-	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427597	*T. m. a.*	Turkey	4	123Z	3	4	;1	*Sr21*
PI 427598	*T. m. a.*	Turkey	3+	2+3Z	3	3+	;1	*Sr21*
PI 427599	*T. m. a.*	Turkey	4	123Z	3	22+	;1	*Sr21*+
PI 427600	*T. m. a.*	Turkey	4	22+Z	3	3+	;1	*Sr21*
PI 427601	*T. m. a.*	Turkey	4	22+Z	3	-	-	*Sr21*
PI 427602	*T. m. a.*	Turkey	4	2+3Z	3	2+3	;1	*Sr21*
PI 427603	*T. m. a.*	Turkey	4	2+3Z	4	3+	;1	*Sr21* *Sr21*
PI 427604	*T. m. a.*	Turkey	3+	1;/3	3	4	;1	*Het*
PI 427605	*T. m. a.*	Turkey	4	12Z	3-	3+	;1	*Sr21*
PI 427606	*T. m. a.*	Turkey	4	12+Z	3	22+/2+3	;1	*Sr21*+
PI 427607	*T. m. a.*	Turkey	4	22+Z	3	2+3	;1	*Sr21*+
PI 427608	*T. m. a.*	Turkey	3+	22+Z	3	3+	;1	*Sr21*
PI 427609	*T. m. a.*	Turkey	-	3+	4	4	-	-
PI 427610	*T. m. a.*	Turkey	4	3	3	3+	;1/2+3	-
PI 427611	*T. m. a.*	Turkey	3+	2+3Z	3	3+	;1	*Sr21*
PI 427612	*T. m. a.*	Turkey	4	22+Z	3	3+	;1	*Sr21*
PI 427613	*T. m. a.*	Turkey	4	23Z/3	3	3+	;1	*Sr21*
PI 427614	*T. m. a.*	Turkey	3+	12Z	3	3+	;1	*Sr21* *Sr21*+
PI 427615	*T. m. a.*	Turkey	3/2+	2+3Z	4	3+	;1	*Het*
PI 427616	*T. m. a.*	Turkey	4	12+Z	3	22+	;1	*Sr21*+
PI 427617	*T. m. a.*	Turkey	4	22+Z	4	22+	;1	*Sr21*+
PI 427618	*T. m. a.*	Turkey	4	12Z	3	22+	;1	*Sr21*+
PI 427619	*T. m. a.*	Turkey	3	-	-	-	-	-
PI 427620	*T. m. a.*	Turkey	4/3	3+	4	4	;1/4	Het
PI 427621	*T. m. a.*	Turkey	4	2-2Z	4	22+	;1	*Sr21*+
PI 427622	*T. m. a.*	Turkey	4	3	3+	2+3	4/;1	Het
PI 427623	*T. m. a.*	Turkey	4	22+Z	4	4	;1	*Sr21*
PI 427624	*T. m. a.*	Turkey	4	3	3	3+	2+3/3+	Het
PI 427625	*T. m. a.*	Turkey	4	-	3	-	-	-
PI 427626	*T. m. a.*	Turkey	4	2+/2+3Z	3	3+	;1+	*Sr21*
PI 427627	*T. m. a.*	Turkey	4	3	4/3	3+	1	*Sr21*
PI 427628	*T. m. a.*	Turkey	-	-	-	-	-	-
PI 427629	*T. m. a.*	Turkey	4	3-	3	4	;1	*Sr21*
PI 427630	*T. m. a.*	Turkey	3	3	4	4	;1	*Sr21*
PI 427631	*T. m. a.*	Turkey	-	-	4	4	;1	-
PI 427632	*T. m. a.*	Turkey	4	3+	4	3+	;1/4	*Het*
PI 427633	*T. m. a.*	Turkey	-	3	3	3+	;1	*Sr21*
PI 427634	*T. m. a.*	Turkey	4	23-	3	3+	;1	*Sr21*
PI 427635	*T. m. a.*	Turkey	3	3+	3	3+	;1	-
PI 427636	*T. m. a.*	Turkey	4	123-Z	4	3+	;1	*Sr21*
PI 427637	*T. m. a.*	Iraq	4	3	4	3+	;1	*Sr21*
PI 427638	*T. m. a.*	Iraq	4	2	3	22+	;1	*Sr21*+
PI 427639	*T. m. a.*	Iraq	3+	4	4	-	-	-
PI 427640	*T. m. a.*	Iraq	3	12Z/123 Z	4	22+	;1	*Sr21*+

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427641	*T. m. a.*	Iraq	3	12+Z	3	22+	;1	*Sr21+*
PI 427642	*T. m. a.*	Iraq	3	123Z	3+	22+	;1	*Sr21+*
PI 427643	*T. m. a.*	Iraq	3+	12+Z/12 3Z	4	22+	;1	*Sr21+*
PI 427644	*T. m. a.*	Iraq	3	12+Z	4	22+	;1	*Sr21+*
PI 427645	*T. m. a.*	Iraq	3	12+Z	3	-	-	*Sr21*
PI 427646	*T. m. a.*	Iraq	3+/3	12+Z	4	3	;1	*Sr21*
PI 427647	*T. m. a.*	Iraq	3+	12+Z	4	3	-	*Sr21*
PI 427648	*T. m. a.*	Iraq	3	22+Z	-	3	-	*Sr21*
PI 427649	*T. m. a.*	Iraq	3	123Z/3	3+	22+	;1	*Sr21*
PI 427650	*T. m. a.*	Iraq	3/3+	12+Z/2+	4	22+/3	;1	*Sr21+ Het*
PI 427651	*T. m. a.*	Iraq	3+	123Z	4	33+	;1	*Sr21*
PI 427652	*T. m. a.*	Iraq	3	12Z	4	22+	;1	*Sr21+*
PI 427653	*T. m. a.*	Iraq	3	-	3	-	-	-
PI 427654	*T. m. a.*	Iraq	3+	12+Z	4	22+	;1	*Sr21+*
PI 427655	*T. m. a.*	Iraq	3	12+Z	3	-	;1	*Sr21*
PI 427656	*T. m. a.*	Iraq	3/3+	12+Z	4	33+	;1	*Sr21*
PI 427657	*T. m. a.*	Iraq	3+	12+Z	3+	22+	;1	*Sr21+*
PI 427658	*T. m. a.*	Iraq	3+	12+Z	4	3+	;1	*Sr21*
PI 427659	*T. m. a.*	Iraq	3+	12Z	3	22+	;1	*Sr21*
PI 427660	*T. m. a.*	Iraq	3	12Z/12+ Z/3	3+	2+3/3	;1	*Sr21+ Het*
PI 427661	*T. m. a.*	Iraq	4	3	4	22+	33+	-
PI 427662	*T. m. a.*	Iraq	4	3+	4	22+	33+	-
PI 427663	*T. m. a.*	Iraq	-	-	-	-	-	-
PI 427664	*T. m. a.*	Iraq	4	12+Z	3+	3+	;1	*Sr21*
PI 427665	*T. m. a.*	Iraq	3	12+Z	3+	3+	;1	*Sr21*
PI 427666	*T. m. a.*	Iraq	3+	123Z	3+	33+	1	*Sr21*
PI 427667	*T. m. a.*	Iraq	3+	123Z	3+	3+	1	*Sr21*
PI 427668	*T. m. a.*	Iraq	-	123Z	3+	-	-	*Sr21*
PI 427669	*T. m. a.*	Iraq	3	23Z	3+	23	12+Z	*Sr21+*
PI 427670	*T. m. a.*	Iraq	-	;12Z	3	3+	;1	*Sr21*
PI 427671	*T. m. a.*	Iraq	4	22+Z	4	4	;1	*Sr21*
PI 427672	*T. m. a.*	Iraq	-	12+Z	3	-	-	*Sr21*
PI 427673	*T. m. a.*	Iraq	4	-	-	3+/2+	;1	-
PI 427674	*T. m. a.*	Iraq	3+	12+Z	3	3+	-	*Sr21*
PI 427675	*T. m. a.*	Iraq	4	12+Z	3+	3	;1	*Sr21*
PI 427676	*T. m. a.*	Iraq	3+	123Z	3	3+	;1	*Sr21*
PI 427677	*T. m. a.*	Iraq	-	12Z	-	-	-	*Sr21*
PI 427678	*T. m. a.*	Iraq	3+	-	-	-	-	-
PI 427679	*T. m. a.*	Iraq	4	123Z	3+	3+	;1	*Sr21*
PI 427680	*T. m. a.*	Iraq	3	123Z	-	-	-	*Sr21*
PI 427681	*T. m. a.*	Iraq	-	-	-	-	-	-
PI 427682	*T. m. a.*	Iraq	4	12+Z	3+	33+	;1	*Sr21*
PI 427683	*T. m. a.*	Iraq	-	12Z	-	-	-	*Sr21*
PI 427684	*T. m. a.*	Iraq	-	12+Z	-	4	-	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427685	*T. m. a.*	Iraq	3	12+Z	3	-	;1	*Sr21*
PI 427686	*T. m. a.*	Iraq	3+	12-Z	3	3	-	*Sr21*
PI 427687	*T. m. a.*	Iraq	4	12Z	3	33+	;1	*Sr21*
PI 427688	*T. m. a.*	Iraq	4	2-	4	4	;1	*Sr21*
PI 427689	*T. m. a.*	Iraq	4	2-	4	4	;1	*Sr21*
PI 427690	*T. m. a.*	Iraq	4	22+Z	4	33+	;1+	*Sr21*
PI 427691	*T. m. a.*	Iraq	4	12Z	4	4	;1	*Sr21*
PI 427692	*T. m. a.*	Iraq	4	12Z	4	4	;1	*Sr21*
PI 427693	*T. m. a.*	Iraq	4	12Z	4	4	;1	*Sr21*
PI 427694	*T. m. a.*	Iraq	4	12Z	4/3+	4	;1	*Sr21*
PI 427695	*T. m. a.*	Iraq	-	12Z	-	-	-	*Sr21*
PI 427696	*T. m. a.*	Iraq	4	12Z	3+	3+	;1	*Sr21*
PI 427697	*T. m. a.*	Iraq	4	12Z	3+	-	-	*Sr21*
PI 427698	*T. m. a.*	Iraq	4	12Z	3+	-	-	*Sr21*
PI 427699	*T. m. a.*	Iraq	4	12Z	3+	-	;1	*Sr21*
PI 427700	*T. m. a.*	Iraq	3+	12Z	4	-	;1+	*Sr21*
PI 427701	*T. m. a.*	Iraq	4	12Z	3+	4	;1	*Sr21*
PI 427702	*T. m. a.*	Iraq	3+	12Z	3	-	;1	*Sr21*
PI 427703	*T. m. a.*	Iraq	4	12Z	3+	-	-	*Sr21*
PI 427704	*T. m. a.*	Iraq	3+	12Z	3+	-	;1	*Sr21*
PI 427705	*T. m. a.*	Iraq	3+	2+3Z	4	33+	1+;	*Sr21*
PI 427706	*T. m. a.*	Iraq	4	12Z	3+	33+	;1	*Sr21*
PI 427707	*T. m. a.*	Iraq	4	-	4	0;	;	-
PI 427708	*T. m. a.*	Iraq	3+	12Z	3	-	;1	*Sr21*
PI 427709	*T. m. a.*	Iraq	3+	12Z	3+	3+	;1	*Sr21*
PI 427710	*T. m. a.*	Iraq	4	12Z	3	3+	;1	*Sr21*
PI 427711	*T. m. a.*	Iraq	4	123Z	4	33+	;1	*Sr21*
PI 427712	*T. m. a.*	Iraq	4	123Z	4	-	;1	*Sr21*
PI 427713	*T. m. a.*	Iraq	4	-	4	-	-	-
PI 427714	*T. m. a.*	Iraq	4	123Z	4	33+	;1	*Sr21*
PI 427715	*T. m. a.*	Iraq	4	123Z	4	13+	1;	*Sr21*+
PI 427716	*T. m. a.*	Iraq	4	123Z	4	33+	;1	*Sr21*
PI 427717	*T. m. a.*	Iraq	4	123Z	4	33+	;1	*Sr21*
PI 427718	*T. m. a.*	Iraq	4	-	4	-	-	-
PI 427719	*T. m. a.*	Iraq	4	123Z/2+	4	3+	;1	*Sr21*
PI 427720	*T. m. a.*	Iraq	4	3/123Z 12+Z/12	4	33+	;1	*Sr21*
PI 427721	*T. m. a.*	Iraq	4	3Z	3+	33+	;1	*Sr21*
PI 427722	*T. m. a.*	Iraq	3+	12+Z	4	33+	;1	*Sr21*
PI 427723	*T. m. a.*	Iraq	4	3/123Z	4	4	;1	*Sr21*
PI 427724	*T. m. a.*	Iraq	4	123Z/3	4	4	;1	*Sr21*
PI 427725	*T. m. a.*	Iraq	4	2+	3+	-	-	*Sr21*
PI 427726	*T. m. a.*	Iraq	4	123Z	4	3+	;1	*Sr21*
PI 427727	*T. m. a.*	Iraq	3+	123Z	4	33+	;1	*Sr21*
PI 427728	*T. m. a.*	Iraq	4	12+Z	4	3+	-	*Sr21*
PI 427729	*T. m. a.*	Iraq	4	123Z	4	3	-	*Sr21*
PI 427730	*T. m. a.*	Iraq	4	2+3Z	4	3+	;1	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427731	*T. m. a.*	Iraq	4	12+Z	4	3+	;1	*Sr21*
PI 427732	*T. m. a.*	Iraq	4	123Z	4	3	-	*Sr21*
PI 427733	*T. m. a.*	Iraq	4	-	4	3+	;1	-
PI 427734	*T. m. a.*	Iraq	-	3	-	-	;1	-
PI 427735	*T. m. a.*	Iraq	4	12+Z	4	33+	;1	*Sr21*
PI 427736	*T. m. a.*	Iraq	4	123Z	3+	4	-	*Sr21*
PI 427737	*T. m. a.*	Iraq	4	2+3Z	3+	4	;1	*Sr21*
PI 427738	*T. m. a.*	Iraq	4	12+Z/2+ 3Z	3+	4	;1	*Sr21*
PI 427739	*T. m. a.*	Iraq	4	123Z	3+	-	-	*Sr21*
PI 427740	*T. m. a.*	Iraq	4	123Z	3	33+	;1	*Sr21*
PI 427741	*T. m. a.*	Iraq	4	123Z	4	4	;1	*Sr21*
PI 427742	*T. m. a.*	Iraq	4	2+3Z/12 +Z/123Z	4	4	;1	*Sr21*
PI 427743	*T. m. a.*	Iraq	4	123Z	4	4	;1	*Sr21*
PI 427744	*T. m. a.*	Iraq	4	12Z	3+	-	;1	*Sr21*
PI 427745	*T. m. a.*	Iraq	4	12	3+	33+	;1	*Sr21*
PI 427746	*T. m. a.*	Iraq	4	12+Z	3+	3+	;1	*Sr21*
PI 427747	*T. m. a.*	Iraq	4	-	-	-	-	-
PI 427748	*T. m. a.*	Iraq	4	12+Z	3+	33+	;1	*Sr21*
PI 427749	*T. m. a.*	Iraq	4	22+Z	3+	33+	;1	*Sr21*
PI 427750	*T. m. a.*	Iraq	4	3	3+	3+	;1	*Sr21*
PI 427751	*T. m. a.*	Iraq	4	12Z	4	3+	;1	*Sr21*
PI 427752	*T. m. a.*	Iraq	4	23Z	3+	2+3	;1	*Sr21*+
PI 427753	*T. m. a.*	Iraq	4	2+	3+	33+	;1	*Sr21*
PI 427754	*T. m. a.*	Iraq	4	12Z	3	3+	;1	*Sr21*
PI 427755	*T. m. a.*	Iraq	4	2+3Z	4	3+	1+;	*Sr21*
PI 427756	*T. m. a.*	Iraq	4	12+Z	3+	3+	;1	*Sr21*
PI 427757	*T. m. a.*	Iraq	4	12	3+	3+	;1	*Sr21*
PI 427758	*T. m. a.*	Iraq	-	12+Z	3	-	-	*Sr21*
PI 427759	*T. m. a.*	Iraq	4	12Z	3+	4	;1	*Sr21*
PI 427760	*T. m. a.*	Iraq	4	2+3Z	3	2+3	1+;	*Sr21*+
PI 427761	*T. m. a.*	Iraq	4	12+Z	4	-	1;	*Sr21*
PI 427762	*T. m. a.*	Iraq	4	2+3Z	4	4	;1	*Sr21*
PI 427763	*T. m. a.*	Iraq	4	123Z	4	3+	;1	*Sr21*
PI 427764	*T. m. a.*	Iraq	3+	12+Z/23 Z	3	-	1+;	*Sr21*
PI 427765	*T. m. a.*	Iraq	3+	12Z	3	33+	1;	*Sr21*
PI 427766	*T. m. a.*	Iraq	4	123Z	3	2+3	;1	*Sr21*+
PI 427767	*T. m. a.*	Iraq	4	12+Z/22 +Z	3	3+	33+	-
PI 427768	*T. m. a.*	Iraq	3+	22+Z/2	4	33+	1;	*Sr21*
PI 427769	*T. m. a.*	Iraq	4	23Z	3	-	-	*Sr21*
PI 427770	*T. m. a.*	Iraq	4	3	4	4	12	*Sr21*
PI 427771	*T. m. a.*	Iraq	4	2+3Z	4	4	1;	*Sr21*
PI 427772	*T. m. a.*	Iraq	3/3+	2+3Z	3+	3+	1;	*Sr21*
PI 427773	*T. m. a.*	Iraq	3+	3+	4	4	1;	-

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427774	*T. m. a.*	Iraq	4	12+Z	4	4	1;	*Sr21*
PI 427775	*T. m. a.*	Iraq	123+Z	2+3Z	3	-	;1	*Sr21*+
PI 427776	*T. m. a.*	Iraq	-	2+3Z	4	-	-	*Sr21* *Sr21*
PI 427777	*T. m. a.*	Iraq	3+	3	4	3+	;1/;1+/3	*Het*
PI 427778	*T. m. a.*	Iraq	4	3	3+	33+	;1	*Sr21*
PI 427779	*T. m. a.*	Iraq	4	-	3+	-	-	-
PI 427780	*T. m. a.*	Iraq	3+	12Z	4	-	;1	*Sr21*
PI 427781	*T. m. a.*	Iraq	3+	123Z	4	3+	1;	*Sr21*
PI 427782	*T. m. a.*	Iraq	3+	123Z	4	33+	;1	*Sr21*
PI 427783	*T. m. a.*	Iraq	3+	12+Z	4	3+	-	*Sr21*
PI 427784	*T. m. a.*	Iraq	3+	123Z 12Z/123	4	13+	;1	*Sr21*+
PI 427785	*T. m. a.*	Iraq	4	Z	4	3+	;1	*Sr21*
PI 427786	*T. m. a.*	Iraq	3+	123Z	4	3+	;1	*Sr21*
PI 427787	*T. m. a.*	Iran	3+	2+3Z 123Z/12	4	-	-	*Sr21*
PI 427788	*T. m. a.*	Iran	4	+Z	4	33+	;1	*Sr21*
PI 427789	*T. m. a.*	Iran	4	23Z	4	33+	;1	*Sr21*
PI 427790	*T. m. a.*	Iran	3	12+Z	3+	33+	;1	*Sr21*
PI 427791	*T. m. a.*	Iran	3	2+3Z	3	-	3+	-
PI 427792	*T. m. a.*	Iran	3+	123Z	4	3+	;1	*Sr21*
PI 427793	*T. m. a.*	Iran	3+	123Z	3+	33+	;1	*Sr21*
PI 427794	*T. m. a.*	Iran	3+	3+	3+	33+	3+/;1	*Het*
PI 427795	*T. m. a.*	Iran	3	3	4	3+	;1	*Sr21*
PI 427796	*T. m. a.*	Iran	3+	1	4	33+	;1	*Sr21*
PI 427797	*T. m. a.*	Iran	4	2+3Z	4	33+	;1	*Sr21*
PI 427798	*T. m. a.*	Iran	4	2+3Z	4	33+	;1	*Sr21*
PI 427799	*T. m. a.*	Iran	4	23Z	4	3+	;1	*Sr21*
PI 427800	*T. m. a.*	Iran	4	23Z	4	3+	;1	*Sr21*
PI 427801	*T. m. a.*	Iran	4	123Z/1	4	4	;1	*Sr21*
PI 427802	*T. m. a.*	Iran	3+	1;	3-	-	;1	*Sr21*
PI 427803	*T. m. a.*	Iran	4	12+Z	3-	33+	;1	*Sr21*
PI 427804	*T. m. a.*	Iran	4	2+3Z	4	3+	;1	*Sr21*
PI 427805	*T. m. a.*	Iran	123+Z	123Z	4	33+	;1	*Sr21*+
PI 427806	*T. m. a.*	Iran	4 4/123+	2+3Z/1	4	-	;1	*Sr21* *Sr21*+
PI 427807	*T. m. a.*	Iran	Z	1	4	4/;1	;1	*Het*
PI 427808	*T. m. a.*	Iran	4	1	4	4	;1	*Sr21*
PI 427809	*T. m. a.*	Iran	-	2+3Z	4	3+	3	-
PI 427810	*T. m. a.*	Iran	3+	123Z 123Z/2+	4	2+3	;1	*Sr21*+
PI 427811	*T. m. a.*	Iran	3+	+3Z	4	33+	;11+	*Sr21*
PI 427812	*T. m. a.*	Iran	3+	123Z 2+3Z/12	4	4	;1	*Sr21*
PI 427813	*T. m. a.*	Iran	3+	+Z	3	3+	;1	*Sr21*
PI 427814	*T. m. a.*	Iran	3+	12Z	4	4	;1	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427815	*T. m. a.*	Iraq	3+	12+Z	4	3+	;1	*Sr21*
PI 427816	*T. m. a.*	Iraq	-	-	-	-	-	-
PI 427817	*T. m. a.*	Iraq	3	-	-	-	-	-
PI 427818	*T. m. a.*	Iraq	3	12Z	3+	-	;1	*Sr21*
PI 427819	*T. m. a.*	Iraq	3+	12Z	-	-	-	*Sr21*
PI 427820	*T. m. a.*	Iraq	3+	123Z	3+	3+	;1	*Sr21*
PI 427821	*T. m. a.*	Iraq	3	12Z	3	33+	;1	*Sr21*
PI 427822	*T. m. a.*	Iraq	3	12Z	3	-	;1	*Sr21*
PI 427823	*T. m. a.*	Iraq	-	12Z	3+	-	;1	*Sr21*
PI 427824	*T. m. a.*	Iraq	3+	22+Z	4	3	;1	*Sr21*
PI 427825	*T. m. a.*	Iraq	3+	123Z	4	3+	;1	*Sr21*
PI 427826	*T. m. a.*	Iraq	3+	22+Z	3	-	;1	*Sr21*
PI 427827	*T. m. a.*	Iraq	4	12Z/2+	3+	4	;1	*Sr21*
PI 427828	*T. m. a.*	Iraq	3+	12+Z	4	4	;1	*Sr21*
PI 427829	*T. m. a.*	Iraq	3+	3	4	33+	;1	*Sr21*
PI 427830	*T. m. a.*	Iraq	3+	12+Z	3	33+	;1	*Sr21*
PI 427831	*T. m. a.*	Iraq	3+	12+Z	3	33+	;1	*Sr21*
PI 427832	*T. m. a.*	Iraq	4	123Z	3	4	;1	*Sr21*
PI 427833	*T. m. a.*	Iraq	3+	123Z	3	33+	;1	*Sr21*
PI 427834	*T. m. a.*	Iraq	3	12+Z	3	-	;1	*Sr21*
PI 427835	*T. m. a.*	Iraq	4	4	3	3+	3+	Sus.
PI 427836	*T. m. a.*	Iraq	4	12+Z/12 3Z	3/4	3+	;1	*Sr21*
PI 427837	*T. m. a.*	Iraq	-	12+Z	3	-	-	*Sr21*
PI 427838	*T. m. a.*	Iraq	4	2+	3	4	;1	*Sr21*
PI 427839	*T. m. a.*	Iraq	3+	-	3	-	-	-
PI 427840	*T. m. a.*	Iraq	4	-	3+	-	-	-
PI 427841	*T. m. a.*	Iraq	4	2+3Z	4	3+	;1	*Sr21*
PI 427842	*T. m. a.*	Iraq	-	2	4	-	-	*Sr21*
PI 427843	*T. m. a.*	Iraq	4	2+3Z	3	4	;1	*Sr21*
PI 427844	*T. m. a.*	Iraq	4	12+Z/12 Z	3	3+	;1	*Sr21*
PI 427845	*T. m. a.*	Iraq	4	12+Z	3	3+	;1	*Sr21*
PI 427846	*T. m. a.*	Iraq	3+	23Z	3	33+	-	*Sr21*
PI 427847	*T. m. a.*	Iraq	4	12+Z	3+	-	;1	*Sr21*
PI 427848	*T. m. a.*	Iraq	4	12+Z/2+	-	-	-	*Sr21*
PI 427849	*T. m. a.*	Iraq	3	12+Z	3	-	;1	*Sr21*
PI 427850	*T. m. a.*	Iraq	4	12+Z	3+	3+	;1	*Sr21*
PI 427851	*T. m. a.*	Iraq	4/3+	12+Z	3	3+	;1	*Sr21*
PI 427852	*T. m. a.*	Iraq	4	12+Z	4	33+	;1	*Sr21*
PI 427853	*T. m. a.*	Iraq	4	12+Z	4	3+	;1	*Sr21*
PI 427854	*T. m. a.*	Iraq	-	-	4	-	-	-
PI 427855	*T. m. a.*	Iraq	4	12+Z	3+	33+	;1-	*Sr21*
PI 427856	*T. m. a.*	Iraq	4	12+Z	4/3	4	;1	*Sr21*
PI 427857	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427858	*T. m. a.*	Iraq	3	12+Z	3	33+	;1	*Sr21*
PI 427859	*T. m. a.*	Iraq	4/3	12+Z	3+/2	33+	;1	*Sr21*+

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427860	*T. m. a.*	Iraq	4	12+Z	4	3+	;1	*Sr21*
PI 427861	*T. m. a.*	Iraq	4	12Z	3+	-	;1	*Sr21*
PI 427862	*T. m. a.*	Iraq	4	123Z	4/3	3+	;1	*Sr21*
PI 427863	*T. m. a.*	Iraq	4	12+Z	2	-	1	*Sr21*+
PI 427864	*T. m. a.*	Iraq	4	123Z	4	3+	;1	*Sr21*
PI 427865	*T. m. a.*	Iraq	4	23Z	4	3+	;1+	*Sr21*
PI 427866	*T. m. a.*	Iraq	3/3+	123Z	3/4	4	;1	*Sr21*
PI 427867	*T. m. a.*	Iraq	3+	123Z	3	4	;1	*Sr21*
PI 427868	*T. m. a.*	Iraq	4	123Z	4/3+	4	;1	*Sr21*
PI 427869	*T. m. a.*	Iraq	4/3	123Z	4	4	;1	*Sr21*
PI 427870	*T. m. a.*	Iraq	3+	22+Z/12 3Z	4	4	1;	*Sr21*
PI 427871	*T. m. a.*	Iraq	4	123Z	4	4	;1	*Sr21*
PI 427872	*T. m. a.*	Iraq	4/3	12+Z	4	4	;1	*Sr21*
PI 427873	*T. m. a.*	Iraq	4/3+	12+Z	4	4	;1	*Sr21*
PI 427874	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427875	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427876	*T. m. a.*	Iraq	4	12+Z/12 3Z	4	4	;1	*Sr21*
PI 427877	*T. m. a.*	Iraq	4	12Z/12+ Z	4	4	;1	*Sr21*
PI 427878	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427879	*T. m. a.*	Iraq	4	12+Z	3/4	3+	;1	*Sr21*
PI 427880	*T. m. a.*	Iraq	4	123Z/2+	4	4	11+	*Sr21*
PI 427881	*T. m. a.*	Iraq	4	12+Z	4	4	11+	*Sr21*
PI 427882	*T. m. a.*	Iraq	4	123Z	4	3+	1	*Sr21*
PI 427883	*T. m. a.*	Iraq	4	123Z	4	3+	;11+	*Sr21*
PI 427884	*T. m. a.*	Iraq	4	12+Z	4	3+	;1	*Sr21*
PI 427885	*T. m. a.*	Iraq	4	12+Z	4	3+	;1	*Sr21*
PI 427886	*T. m. a.*	Iraq	4	123Z	4	4	;1	*Sr21*
PI 427887	*T. m. a.*	Iraq	4	2	-	-	-	*Sr21*
PI 427888	*T. m. a.*	Iraq	4	12+Z/2+ 3Z	4	3+	12	*Sr21*
PI 427889	*T. m. a.*	Iraq	4	12+Z/2+	4	3+	12	*Sr21*
PI 427890	*T. m. a.*	Iraq	4	12Z	4	-	-	*Sr21*
PI 427891	*T. m. a.*	Iraq	4	123Z	4	3+	12	*Sr21*
PI 427893	*T. m. a.*	Iraq	4	123Z/2+/ 3	4	3+	;1	*Sr21*
PI 427894	*T. m. a.*	Iraq	4	123Z/12 +Z	4	3+	-	*Sr21*
PI 427895	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427896	*T. m. a.*	Iraq	4	123Z	4	4	;1	*Sr21*
PI 427897	*T. m. a.*	Iraq	4	123Z	4	4	;1	*Sr21*
PI 427898	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427899	*T. m. a.*	Iraq	4	123Z	4	4	1	*Sr21*
PI 427900	*T. m. a.*	Iraq	3	22+Z/2+/ 123Z	4	-	-	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427901	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427902	*T. m. a.*	Iraq	4	22+Z	4	4	;1	*Sr21*
PI 427903	*T. m. a.*	Iraq	4	123Z	4	4	;1	*Sr21*
PI 427904	*T. m. a.*	Iraq	4	3	4	4	12	*Sr21*
PI 427905	*T. m. a.*	Iraq	4	2+	4	4	;1	*Sr21*
PI 427906	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427907	*T. m. a.*	Iraq	4	12+Z	4	3+	;1	*Sr21*
PI 427908	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427909	*T. m. a.*	Iraq	-	12+Z	4	-	-	*Sr21*
PI 427910	*T. m. a.*	Iraq	-	12Z	-	-	-	*Sr21*
PI 427911	*T. m. a.*	Iraq	4	12Z	4	3+	;1	*Sr21*
PI 427912	*T. m. a.*	Iraq	4	12Z	4	3+	;1	*Sr21*
PI 427913	*T. m. a.*	Iraq	4	12-Z	4	3+	;1	*Sr21*
PI 427914	*T. m. a.*	Iraq	4	123Z	4	4	;1	*Sr21*
PI 427915	*T. m. a.*	Iraq	4	12Z	4	4	;1	*Sr21*
PI 427916	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427918	*T. m. a.*	Iraq	4	3	4	4	11+	*Sr21*
PI 427919	*T. m. a.*	Iraq	4	3	4	-	-	-
PI 427920	*T. m. a.*	Iraq	-	12+Z	4	4	;1	*Sr21*
PI 427921	*T. m. a.*	Iraq	4	123Z	4	3+	;1	*Sr21*
PI 427922	*T. m. a.*	Iraq	3	23Z	4	-	;1	*Sr21*
PI 427923	*T. m. a.*	Iraq	4	23Z	4	4	13-	*Sr21*
PI 427924	*T. m. a.*	Iraq	4	2+3Z	4	4	11+	*Sr21*
PI 427925	*T. m. a.*	Iraq	4	2+3Z	4	4	;1	*Sr21*
PI 427926	*T. m. a.*	Iraq	4	2+3Z	4	-	-	*Sr21*
PI 427928	*T. m. a.*	Iraq	-	-	-	-	-	-
PI 427929	*T. m. a.*	Iraq	-	2+3Z	4	-	-	*Sr21*
PI 427930	*T. m. a.*	Iraq	-	123Z	3	-	-	*Sr21*
PI 427931	*T. m. a.*	Iraq	4	123Z	4	4	;1	*Sr21*
PI 427932	*T. m. a.*	Iraq	3+	12+Z	3/2+	4	;1	*Sr21*+
PI 427933	*T. m. a.*	Iraq	3+	12Z	3+	4	;1	*Sr21*
PI 427934	*T. m. a.*	Iraq	4	12Z/12+ Z	4	4	;1	*Sr21*
PI 427935	*T. m. a.*	Turkey	4	123Z	3+	3+	;1	*Sr21*
PI 427936	*T. m. a.*	Iraq	4	12+Z	3+	33+	;1	*Sr21*
PI 427937	*T. m. a.*	Iraq	4	3+	4	33+	4	Sus.
PI 427938	*T. m. a.*	Iraq	4	123Z	-	-	-	*Sr21*
PI 427939	*T. m. a.*	Iraq	4	2+3Z	4	4	;1	*Sr21*
PI 427940	*T. m. a.*	Iraq	4	12+Z	4	3+	;1	*Sr21*
PI 427941	*T. m. a.*	Iraq	4	2-2+Z	4	4	;1	*Sr21*
PI 427942	*T. m. a.*	Iraq	4	2+3Z	3+	33+	;1	*Sr21*
PI 427943	*T. m. a.*	Iraq	4	12+Z	3+	33+	;1	*Sr21*
PI 427944	*T. m. a.*	Iraq	4	12+Z	4	3+	;1	*Sr21*
PI 427945	*T. m. a.*	Iraq	4	12+Z/12 3Z	4	3+	;1	*Sr21*
PI 427946	*T. m. a.*	Iraq	4	12+Z/12 3Z	4	4	;1	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427947	*T. m. a.*	Iraq	4	23Z	4	4	;1	*Sr21*
PI 427948	*T. m. a.*	Iraq	4	2+3Z	4	3+	;1	*Sr21*
PI 427949	*T. m. a.*	Iraq	4	-	4	4	;1	*Sr21*
PI 427950	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427951	*T. m. a.*	Iraq	3/4	123Z	4	4	;1	*Sr21*
PI 427952	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427953	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427954	*T. m. a.*	Iraq	4	12Z/2+	3	4	;1	*Sr21*
PI 427955	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427956	*T. m. a.*	Iraq	4	12Z/123 Z	4	4	;1	*Sr21*
PI 427957	*T. m. a.*	Iraq	4	4/123Z	4	4	3+/;1	*Sr21 Het*
PI 427958	*T. m. a.*	Iraq	4	12Z	4	4	;1	*Sr21*
PI 427960	*T. m. a.*	Iraq	4	12+Z	4	3+	;1	*Sr21*
PI 427961	*T. m. a.*	Iraq	4	12+Z	4	4	;1	*Sr21*
PI 427962	*T. m. a.*	Iraq	4	12+Z	4	3+	;1	*Sr21*
PI 427963	*T. m. a.*	Turkey	4	4	-	3+	4	*Sus.*
PI 427964	*T. m. a.*	Turkey	2+3	123Z	4	3+	;1	*Sr21+*
PI 427965	*T. m. a.*	Turkey	4	1	4	33+	;1	*Sr21*
PI 427966	*T. m. a.*	Turkey	4	123Z/2+ 3Z	4	4	;1	*Sr21*
PI 427967	*T. m. a.*	Turkey	4/3	12+Z/12 3Z	4	4	;1	*Sr21*
PI 427968	*T. m. a.*	Turkey	3+	12+Z	3+	3+	;1	*Sr21*
PI 427969	*T. m. a.*	Turkey	4	2+	3+	3+	;11+	*Sr21*
PI 427970	*T. m. a.*	Turkey	3+	3	4	3+	;1	*Sr21*
PI 427971	*T. m. a.*	Turkey	4	3	4	4	3+	*Sus.*
PI 427972	*T. m. a.*	Turkey	123Z	12Z	4	;1	;1	-
PI 427973	*T. m. a.*	Turkey	4	2-	4	-	-	*Sr21*
PI 427974	*T. m. a.*	Turkey	4	12Z	4	3+	;1	*Sr21*
PI 427975	*T. m. a.*	Turkey	4	123Z	4	4	;1	*Sr21*
PI 427976	*T. m. a.*	Turkey	3+	2+3Z	2+	3+	;1	*Sr21+*
PI 427977	*T. m. a.*	Turkey	4	12Z/12+ Z	4	33+	;1	*Sr21*
PI 427978	*T. m. a.*	Turkey	4	2+3Z	4	33+	;1	*Sr21*
PI 427979	*T. m. a.*	Turkey	23Z	123Z	3	-	-	*Sr21+*
PI 427980	*T. m. a.*	Turkey	4	12+Z	4	3+	;1	*Sr21*
PI 427981	*T. m. a.*	Turkey	4	12+Z/12 3Z	4	4	;1	*Sr21*
PI 427982	*T. m. a.*	Turkey	2-	1;	2	;1	;1	*Sr22*
PI 427983	*T. m. a.*	Turkey	4	3	4	4	;1	*Sr21*
PI 427984	*T. m. a.*	Turkey	4	2+	3+	4	;1	*Sr21 Sr22*
PI 427986	*T. m. a.*	Turkey	2-	1;/3	2-	;1	;1	*Het*
PI 427987	*T. m. a.*	Turkey	4	1;	4	4	;1	*Sr21*
PI 427988	*T. m. a.*	Turkey	2-2	12+Z	2-	2-	;1	*Sr22*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 427989	*T. m. a.*	Turkey	4	12Z	4	4	-	*Sr21*
PI 427990	*T. m. a.*	Lebanon	4	12+Z	3+	4	;1+	*Sr21*
PI 427991	*T. m. a.*	Lebanon	4	2-2Z	3+	-	-	*Sr21*
PI 427992	*T. m. a.*	Lebanon	4	12+Z 123Z/1;/	3	4	-	*Sr21*
PI 427993	*T. m. a.*	Lebanon	4	12Z	4	4	;1	*Sr21*
PI 427994	*T. m. a.*	Lebanon	4	12+Z	4	4	;1+	*Sr21*
PI 427995	*T. m. a.*	Lebanon	4	12+Z	4	4	;/+	*Sr21* *Sr21*
PI 427996	*T. m. a.*	Lebanon	4	12+Z	3	4	33+/;1	*Het*
PI 427997	*T. m. a.*	Lebanon	4	2+	3+	4	12	*Sr21*
PI 427999	*T. m. a.*	Lebanon	4	3	3	4	-	- *Sr21*
PI 428000	*T. m. a.*	Lebanon	4	12Z	4	4	12/3+	*Het*
PI 428001	*T. m. a.*	Lebanon	4	12Z	-	-	-	*Sr21*
PI 428002	*T. m. a.*	Lebanon	4	-	3+	4	12/23+Z	*Sr21*
PI 428003	*T. m. a.*	Turkey	4	2+/12+ 1/12+Z/1	4	-	-	*Sr21*
PI 428004	*T. m. a.*	Turkey	3+	2-Z	4	4	;1	*Sr21*
PI 428005	*T. m. a.*	Iraq	4	-	3+	3+	;1+	*Sr21*
PI 428006	*T. m. a.*	Iraq	-	1	-	-	-	-
PI 428007	*T. m. a.*	Iraq	3+	1/2+	3+	3+	;1	*Sr21*
PI 428008	*T. m. a.*	Turkey	4	123Z	4	4	;1	*Sr21*
PI 428009	*T. m. a.*	Azerbaijan	3+	12+Z	3+	4	;1	*Sr21*
PI 428010	*T. m. a.*	Azerbaijan	4	23Z	4	4	;1+	*Sr21*
PI 428011	*T. m. a.*	Azerbaijan	3+	23Z	4	4	;1	*Sr21*
PI 428012	*T. m. a.*	Armenia	4	12+Z	3	4	;1	*Sr21*
PI 428076	*T. m. a.*	Turkey	4	3	4	4	;1	*Sr21*
PI 470712	*T. m. a.*	Turkey	123Z	12+Z	4	23+2	;1-	*Sr21*+
PI 470713	*T. m. a.*	Turkey	123Z	12+Z	4	23+2	;1	*Sr21*+
PI 470714	*T. m. a.*	Turkey	123Z	12+Z	3+	23+2	;1	*Sr21*+
PI 470715	*T. m. a.*	Turkey	123Z	12+Z/1	3+/4	23+2	;1	*Sr21*+
PI 470716	*T. m. a.*	Turkey	23Z	2+	4	4	;1+	*Sr21*+
PI 470717	*T. m. a.*	Turkey	23Z	12+Z	4	4	;1+	*Sr21*+
PI 470718	*T. m. a.*	Turkey	23Z	2+	4	3+	;1	*Sr21*+ *Sr22*
PI 470719	*T. m. a.*	Turkey	3+/2	2/3	2/3	4/2	4/;1	*Het* *Sr22*
PI 470720	*T. m. a.*	Turkey	2/3	1	2	2-	;1	*Het*
PI 470721	*T. m. a.*	Turkey	2	1	2	2-2	12	*Sr22* *Sr22*
PI 470722	*T. m. a.*	Turkey	2/3+	1;/3	2/4	2-	;1	*Het*
PI 470723	*T. m. a.*	Turkey	2	1	2	2-	;1	*Sr22*
PI 470724	*T. m. a.*	Turkey	2	1	-	-	2-	*Sr22* *Sr22*
PI 470725	*T. m. a.*	Turkey	2/3+	12Z/1	3/2	4/2+	2-	*Het*
PI 470726	*T. m. a.*	Turkey	3+	2+	4	3+	12	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 470727	*T. m. a.*	Turkey	3+	4	3+	3+	3+	Sus.
PI 470728	*T. m. a.*	Turkey	3+	2+3Z	3+	3+	;1	*Sr21*
PI 487249	*T. m. a.*	Syria	4	2+/3/12+ Z	3+	4	;1	*Sr21*
PI 503299	*T. m. a.*	Turkey	3+	12Z	3	4	;1	*Sr21*
PI 503300	*T. m. a.*	Turkey	3+	3	3	-	;1+	*Sr21*
PI 503301	*T. m. a.*	Turkey	4	12Z	3+	4	;1	*Sr21*
PI 503302	*T. m. a.*	Turkey	123Z	22+Z	3+	4	;1	*Sr21*
PI 503303	*T. m. a.*	Turkey	3+	2+3Z/12 +Z/3	3+	4	;1	*Sr21*
PI 503304	*T. m. a.*	Turkey	3	2+/12+Z	3	4	-	*Sr21*
PI 503305	*T. m. a.*	Iraq	3/3+	2	4	4	;1	*Sr21*
PI 503306	*T. m. a.*	Iraq	4	2/2+	3+	4	;1	*Sr21*
PI 503307	*T. m. a.*	Iraq	4	2+	3+	4	;1	*Sr21*
PI 503308	*T. m. a.*	Iraq	3+	2+3Z	3+	4	33+	-
PI 503309	*T. m. a.*	Iran	3+	12+/22+	23Z/3+	4	;1	*Sr21*+
PI 503578	*T. m. a.*	Iran	4	1;	3+	4	;1-	*Sr21*
PI 537998	*T. m. a.*	Turkey	4	123Z	4	4	;1	*Sr21*
PI 538001	*T. m. a.*	Turkey	4	1/12+Z	23Z	33+	;1	*Sr21*+
PI 538002	*T. m. a.*	Turkey	4	2+3Z	4	3+	;1	*Sr21*
PI 538510	*T. m. a.*	Iraq	4/3+	12+Z	4	4	;1	*Sr21*
PI 538524	*T. m. a.*	Turkey	3	23Z	4/3	4	;1	*Sr21*
PI 538525	*T. m. a.*	Turkey	-	12Z	-	4	;1	*Sr21*
PI 538526	*T. m. a.*	Turkey	4/3	3	4	3+	;1	*Sr21*
PI 538527	*T. m. a.*	Turkey	4/3+	1/12	3+	3+	;1	*Sr21*
PI 538528	*T. m. a.*	Turkey	3/2	2	3+	-	;1	*Sr21*
PI 538529	*T. m. a.*	Turkey	4/3	2+3Z	3+	3+	23+Z	*Sr21*
PI 538530	*T. m. a.*	Turkey	3	3+	4	3+	3+	Sus.
PI 538531	*T. m. a.*	Turkey	3+	22+Z	4	3+	;1	*Sr21*
PI 538532	*T. m. a.*	Turkey	3	-	4	3+	-	-
PI 538533	*T. m. a.*	Turkey	3	2-	3+	3+	-	*Sr21*
PI 538534	*T. m. a.*	Turkey	3+	2-	3+	3+	;1	*Sr21*
PI 538535	*T. m. a.*	Turkey	3	2-	3+	3+	;1	*Sr21*
PI 538536	*T. m. a.*	Turkey	3	2-/23-Z	3+	4	-	*Sr21*
PI 538537	*T. m. a.*	Turkey	3	2-	3+	-	;1	*Sr21*
PI 538538	*T. m. a.*	Turkey	3	-	-	-	;1	*Sr21*
PI 538539	*T. m. a.*	Turkey	-	-	-	-	-	-
PI 538540	*T. m. a.*	Turkey	4	33+	4	4	4	Sus.
PI 538541	*T. m. a.*	Turkey	-	2+	4	-	-	*Sr21*
PI 538542	*T. m. a.*	Iraq	-	-	-	-	-	-
PI 538543	*T. m. a.*	Iraq	3+	2-	3/3+	3+	;1	*Sr21*
PI 538544	*T. m. a.*	Iraq	4	12-	4	3+	;1	*Sr21*
PI 538545	*T. m. a.*	Iraq	4	11+	4	4	;1	*Sr21*
PI 538546	*T. m. a.*	Iraq	4	3+	4	4	3+	Sus.
PI 538547	*T. m. a.*	Iraq	4	2	3+	4	;1-	*Sr21*
PI 538548	*T. m. a.*	Iraq	4	3	4	4	123Z	-
PI 538549	*T. m. a.*	Iraq	4	123-Z	4	4	;1	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 538550	*T. m. a.*	Iraq	4	22+Z	3+	3+	;1	*Sr21*
PI 538551	*T. m. a.*	Iraq	4/3	2-	3+	4	;1/3	*Sr21* *Het*
PI 538552	*T. m. a.*	Iraq	4/3+	3+	4	3+	3+	Sus.
PI 538553	*T. m. a.*	Iraq	3+	2-2	4	4	;1	*Sr21*
PI 538554	*T. m. a.*	Iraq	4	2+3	4	4	;1	*Sr21*
PI 538555	*T. m. a.*	Iraq	4	3	4	-	-	-
PI 538556	*T. m. a.*	Iraq	4	-	4	4	1;	*Sr21*
PI 538557	*T. m. a.*	Iraq	3+	2+3-Z	3+	4	;1	*Sr21*
PI 538558	*T. m. a.*	Iraq	3+	3-	3+	-	;1	*Sr21*
PI 538559	*T. m. a.*	Iraq	3+	2+	3+	4	-	*Sr21*
PI 538560	*T. m. a.*	Iraq	3	22+	-	-	-	*Sr21*
PI 538561	*T. m. a.*	Iraq	3+	2	3+	-	-	*Sr21*
PI 538562	*T. m. a.*	Iraq	3+	-	4/3	-	-	-
PI 538563	*T. m. a.*	Iraq	4	3/2	3/3+	-	-	*Sr21*
PI 538564	*T. m. a.*	Iraq	3	4	-	-	;1+	-
PI 538565	*T. m. a.*	Iraq	3+	3	3	-	-	-
PI 538566	*T. m. a.*	Iraq	3+	-	3	4	-	-
PI 538567	*T. m. a.*	Iraq	-	2	3+	4	-	*Sr21*
PI 538568	*T. m. a.*	Iraq	3	3-	3+	-	-	-
PI 538569	*T. m. a.*	Iraq	3+	2+3	3	-	-	*Sr21*
PI 538570	*T. m. a.*	Iraq	3+	22+Z	3+	4	-	*Sr21*
PI 538571	*T. m. a.*	Iraq	3+	3	-	-	-	-
PI 538572	*T. m. a.*	Iraq	3+	3-	4	-	-	-
PI 538573	*T. m. a.*	Iraq	4	2+3-	3+	-	-	*Sr21*
PI 538574	*T. m. a.*	Iraq	3+	22+	3	4	;1	*Sr21*
PI 538575	*T. m. a.*	Iraq	3+	22+Z	-	4	-	*Sr21*
PI 538576	*T. m. a.*	Iran	3+	3	3	4	-	-
PI 538577	*T. m. a.*	Iran	3+	3	3	-	33+	-
PI 538579	*T. m. a.*	Iraq	4	2+3	4	4	;1	*Sr21*
PI 538580	*T. m. a.*	Iraq	4	2+	2+	4	;1	*Sr21*+
PI 538581	*T. m. a.*	Iraq	3+	2+	3+	4	;1	*Sr21*
PI 538582	*T. m. a.*	Iraq	3	2+	3	-	-	*Sr21*
PI 538583	*T. m. a.*	Iraq	3+	3-	3	-	3+	-
PI 538584	*T. m. a.*	Iraq	3+	-	-	-	;1	*Sr21*
PI 538585	*T. m. a.*	Iraq	3+	22+	3	-	-	*Sr21*
PI 538586	*T. m. a.*	Iraq	3+	-	-	-	-	-
PI 538587	*T. m. a.*	Iraq	3+	2+3	3+	4	;1+	*Sr21*
PI 538588	*T. m. a.*	Iraq	3+	2+3	3	-	-	*Sr21*
PI 538589	*T. m. a.*	Iraq	3+	3-3	3+	-	-	-
PI 538590	*T. m. a.*	Iraq	4	2+3-Z	3+	4	;1	*Sr21*
PI 538591	*T. m. a.*	Iraq	-	22+Z	4	-	-	*Sr21* *Sr21*+
PI 538592	*T. m. a.*	Iraq	4	2+3-Z	4/2++	4	;1	*Het*
PI 538593	*T. m. a.*	Iraq	3+	2	4	-	-	*Sr21*
PI 538594	*T. m. a.*	Iraq	3+	22+Z	4	4	;1	*Sr21*
PI 538595	*T. m. a.*	Iraq	3+	22+	3+	4	;1	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
								Sr21
PI 538596	*T. m. a.*	Iraq	3	2+3Z	4	4	;1/4	*Het*
PI 538597	*T. m. a.*	Iraq	4	22+	4	4	;1	*Sr21*
PI 538598	*T. m. a.*	Iraq	3	2+3Z	3+	3+	;1+	*Sr21*
PI 538599	*T. m. a.*	Iraq	-	3+	4	-	-	-
PI 538600	*T. m. a.*	Iraq	3	3-	4	4	-	-
PI 538601	*T. m. a.*	Iraq	-	2+3	3+	4	-	*Sr21*
PI 538602	*T. m. a.*	Iraq	3+	3+	4	-	;1+	-
PI 538603	*T. m. a.*	Iraq	3+	3	3+	4	;1+	*Sr21*
PI 538604	*T. m. a.*	Iraq	4	2+3-	3+	4	-	*Sr21*
PI 538605	*T. m. a.*	Iraq	3+/3	-	3	-	-	-
PI 538606	*T. m. a.*	Iraq	3+	12Z	3	4	-	*Sr21*
PI 538607	*T. m. a.*	Turkey	3/3+	3+	3+	3+	4	Sus.
PI 538608	*T. m. a.*	Turkey	3	2+3-	3	4	12	*Sr21*
PI 538609	*T. m. a.*	Iraq	3+	22+	3	3+	;1	*Sr21*
PI 538610	*T. m. a.*	Iraq	3+	2+3-	3+	3+	;1	*Sr21*
PI 538611	*T. m. a.*	Iraq	3+	2+3-	4	4	;1	*Sr21*
PI 538612	*T. m. a.*	Iraq	4	2+3-	4/3+	4	;1	*Sr21*
PI 538613	*T. m. a.*	Iraq	3/3+	2+3-Z	3	-	-	*Sr21*
PI 538614	*T. m. a.*	Iraq	3+	22+	3+	-	;1+	*Sr21*
PI 538615	*T. m. a.*	Iraq	3+	2+	3+	4	;1	*Sr21*
PI 538616	*T. m. a.*	Iraq	3+	2+	3+	4	;1	*Sr21*
PI 538617	*T. m. a.*	Iraq	3+/4	22+	4	4	;1	*Sr21*
PI 538619	*T. m. a.*	Turkey	4	22+	3+	4	;1	*Sr21*
PI 538620	*T. m. a.*	Turkey	3+	-	4	-	-	-
PI 538621	*T. m. a.*	Turkey	3+	2+	4	4	;1	*Sr21*
PI 538622	*T. m. a.*	Turkey	4	2-	4	4	4	-
PI 538623	*T. m. a.*	Turkey	3+/3	22+Z	3+/3	-	-	*Sr21*
PI 538624	*T. m. a.*	Turkey	2-	2-	2	2-	;1	*Sr22*
								Sr21+
PI 538625	*T. m. a.*	Turkey	2/3	22+Z/1	3	3	-	*Het*
PI 538720	*T. m. a.*	Turkey	3+	12+Z	4	4	;1	*Sr21*
PI 538723	*T. m. a.*	Turkey	3+	22+Z	-	-	;1	*Sr21*
		United						
PI 542475	*T. m. a.*	States	3+	3+	3+	4	;1	-
PI 554479	*T. m. a.*	Turkey	3+/4	3+/2+	4	4	4	Het
PI 554480	*T. m. a.*	Turkey	3+/3	3-	3	;1	;1+	*Sr21*+
								Sr21
PI 554481	*T. m. a.*	Turkey	3+	3/2+	3/3+	3+	;1	*Het*
PI 554482	*T. m. a.*	Turkey	3+	22+Z	3+	4	;1	*Sr21*
PI 554483	*T. m. a.*	Turkey	3/3+	2+	3+	3+	;1	*Sr21*
PI 554484	*T. m. a.*	Turkey	3	2+/1	3	4	;1	*Sr21*
PI 554485	*T. m. a.*	Turkey	3+	2+	3/4	4	;1	*Sr21*
PI 554486	*T. m. a.*	Turkey	3+	22+/2+3	3+	4	;1	*Sr21*
PI 554487	*T. m. a.*	Turkey	3+	2+	3	3+	;1+	*Sr21*
PI 554488	*T. m. a.*	Turkey	2+3	3-	3+	3+/4	;1+	*Sr21*+
PI 554490	*T. m. a.*	Turkey	3	12	3	3+	;1	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 554491	*T. m. a.*	Turkey	3+	2+3-	3+	3+	23	*Sr21*
PI 554492	*T. m. a.*	Turkey	3+	3+/2-	3+	4	4	*Sr21 Het*
PI 554493	*T. m. a.*	Turkey	3	2-/3-	3+	3+/4	;1	*Sr21*
PI 554494	*T. m. a.*	Turkey	3	1;	3+	22+	;1	*Sr21*+
PI 554495	*T. m. a.*	Turkey	3	23-Z	3	3+	;1	*Sr21*
PI 554496	*T. m. a.*	Turkey	3	22+	3+	3+	;1	*Sr21*
PI 554497	*T. m. a.*	Turkey	3	22+	3+	3+	;1	*Sr21*
PI 554498	*T. m. a.*	Turkey	3+	1/3+	3+	4	4	*Het*
PI 554499	*T. m. a.*	Turkey	3	3-/23-Z	3+	3	33+	-
PI 554500	*T. m. a.*	Turkey	3+/3	1	3+	3+	;1-	*Sr21*
PI 554501	*T. m. a.*	Turkey	3	22+	3+	33+	;1	*Sr21*
PI 554502	*T. m. a.*	Turkey	3+/3	2-2	3+/3	3+	;1	*Sr21*
PI 554503	*T. m. a.*	Turkey	3+	2+3-	3/3+	3+	;1	*Sr21*
PI 554504	*T. m. a.*	Turkey	3/3+	2+3Z	3	3+	;1+	*Sr21*
PI 554505	*T. m. a.*	Turkey	4	2+3	3+	3+	;1	*Sr21*
PI 554506	*T. m. a.*	Turkey	-	2+3	3	4	3+	-
PI 554507	*T. m. a.*	Turkey	3+	3	3	4	4	Sus. *Sr21*
PI 554508	*T. m. a.*	Turkey	3+	22+	3+	3	;1/3	*Het* *Sr21*
PI 554509	*T. m. a.*	Turkey	3+	22+/3	3	33+	;1/3+	*Het*
PI 554510	*T. m. a.*	Turkey	3+	2	3	33+	;1	*Sr21*
PI 554511	*T. m. a.*	Turkey	-	3-	3+	3+	-	-
PI 554512	*T. m. a.*	Turkey	3+	3	3+	3+	1+3-	-
PI 554514	*T. m. a.*	Former USSR	3+	3-	3+	3+	;1	*Sr21*
PI 554516	*T. m. a.*	Turkey	3+	3-	3+	3+	;1	*Sr21*
PI 554517	*T. m. a.*	Former USSR	2-	1	2-	;2-	;1	*Sr22*
PI 554518	*T. m. a.*	Former USSR	3+	2+3-Z	3+	4	;1	*Sr21*
PI 554519	*T. m. a.*	Former USSR	3+	3+	3+	4	4	*Sus.*
PI 554520	*T. m. a.*	USSR	3	3-	3	4	;1+	*Sr21*
PI 554521	*T. m. a.*	Turkey	2/23Z	;1/12Z	3	;2-	;	-
PI 554522	*T. m. a.*	Turkey	3	23-/1	3	4	;1	*Sr21* *Sr21*+
PI 554523	*T. m. a.*	Turkey	3/2-	22+	3	4	;1	*Het*
PI 554524	*T. m. a.*	Turkey	2-	1	2-	;2=	;1	*Sr22*
PI 554526	*T. m. a.*	Turkey	2	2	3	23	;1	-
PI 554530	*T. m. a.*	Turkey	2-	2-	3	;1	;1	-
PI 554531	*T. m. a.*	Turkey	3	22+	3	3+	;1	*Sr21*
PI 554532	*T. m. a.*	Turkey	3+	3	4	4	;1	*Sr21*
PI 554533	*T. m. a.*	Turkey	4	22+/3	3+	4	;1	*Sr21*
PI 554534	*T. m. a.*	Turkey	3+	123Z	3+	4	;1	*Sr21*
PI 554535	*T. m. a.*	Turkey	3+	22+/3-	3	4	;1	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 554537	*T. m. a.*	Turkey	4	22+	3+	4	-	*Sr21*
PI 554538	*T. m. a.*	Turkey	4	22+3Z	3+/2	4/2	;1	*Sr21+ Het*
PI 554539	*T. m. a.*	Turkey	3+	22+	3+/2+	3+	1+	*Sr21+ Het*
PI 554541	*T. m. a.*	Turkey	3+	2	3+	4	;1	*Sr21*
PI 554542	*T. m. a.*	Turkey	3	22+	3+	4	;1+	*Sr21*
PI 554543	*T. m. a.*	Turkey	2	1	2	2-	;1-	*Sr22*
PI 554544	*T. m. a.*	Turkey	4/2	22+3	4/3	3+/1+2	;1	*Sr21+ Het*
PI 554545	*T. m. a.*	Turkey	2-	1	2	2-	;1	*Sr22*
PI 554546	*T. m. a.*	Turkey	2-	2-	2-	;2-	;1-	*Sr22*
PI 554547	*T. m. a.*	Turkey	2	2	2	22+	;1	*Sr22*
PI 554548	*T. m. a.*	Turkey	2	2-	2	2+	;1	*Sr22*
PI 554549	*T. m. a.*	Turkey	2	2-	2	22+	;1	*Sr22*
PI 554551	*T. m. a.*	Turkey	2-/;12-	2-	2/2+	2-	;1-	*Sr22*
PI 554552	*T. m. a.*	Turkey	2-	;2-	2	2-	;1	*Sr22*
PI 554553	*T. m. a.*	Turkey	2-	;1	2-	2-	;1-	*Sr22*
PI 554554	*T. m. a.*	Turkey	2-	1-	2	23	;1	*Sr22*
PI 554555	*T. m. a.*	Turkey	2/3	;1-	2	2	;1	*Sr22 Het*
PI 554556	*T. m. a.*	Turkey	3+	2-	22+	4	;1	*Sr21+*
PI 554557	*T. m. a.*	Turkey	;12-	;2-	2	;2-	;1	*Sr22*
PI 554558	*T. m. a.*	Turkey	2-	2-	2-	-	;2-	*Sr22*
PI 554560	*T. m. a.*	Turkey	2-/3	1	2	;2-	;2-	*Sr22 Het*
PI 554561	*T. m. a.*	Turkey	3+	2+3Z	3+	23	;1	*Sr21+*
PI 554562	*T. m. a.*	Turkey	;123	3	3	3+	;1/1+3-	*Sr21+*
PI 554563	*T. m. a.*	Turkey	3+	2+3	2+3	4	12	*Sr21+*
PI 554564	*T. m. a.*	Turkey	3+	3-	2+3	4	12	*Sr21+*
PI 554565	*T. m. a.*	Turkey	-	3-	-	4	12	*Sr21*
PI 554566	*T. m. a.*	Turkey	2-	2-	2	2	;1	*Sr22*
PI 554567	*T. m. a.*	Turkey	;12-	1	2	2-	;1	*Sr22*
PI 554568	*T. m. a.*	Turkey	3+	22+	3	4/3	;1	*Sr21*
PI 554569	*T. m. a.*	Turkey	3/3+	22+	2+3	3+	;1	*Sr21+*
PI 554570	*T. m. a.*	Turkey	3+	2-	3	4	;1	*Sr21*
PI 554571	*T. m. a.*	Turkey	3+	22+	3+	4	;1	*Sr21*
PI 554572	*T. m. a.*	Turkey	3+/2-	2+3Z	3	4	;1	*Sr21+ Het*
PI 554573	*T. m. a.*	Turkey	3+	2+3-Z	3	4	;1	*Sr21*
PI 554574	*T. m. a.*	Turkey	3+	2/2+	3+/3	4	;1	*Sr21*
PI 554575	*T. m. a.*	Turkey	3+	22+	3	4	;1	*Sr21*
PI 554576	*T. m. a.*	Turkey	3+	22+	3	4	;1	*Sr21*
PI 554577	*T. m. a.*	Turkey	3+	2+3-	3	4	12	*Sr21*
PI 560724	*T. m. a.*	Turkey	4	2+3-	3+	4	;1	*Sr21*
PI 560729	*T. m. a.*	Turkey	3+	2+3-	3	4	;1	*Sr21*
PI 560864	*T. m. a.*	Turkey	3+	22+	3	4	;1	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 560865	*T. m. a.*	Turkey	4/3+	3/1	3+/3	4	;1	*Sr21*
PI 560866	*T. m. a.*	Turkey	3+	3-	3	4	12	*Sr21*
PI 560867	*T. m. a.*	Turkey	3+	3-	3	3+	12+	*Sr21*
PI 560868	*T. m. a.*	Turkey	3+	3-	3	4	11+	*Sr21*
PI 560869	*T. m. a.*	Turkey	3	2+3Z	3	4	;1	*Sr21*
PI 573517	*T. m. a.*	Turkey	2-/3	2-/2+	3/2-	4	;1	*Sr21+ Het*
PI 573518	*T. m. a.*	Turkey	2-	2-	2	;1-	;1	*Sr22*
PI 573520	*T. m. a.*	Turkey	12-	2-	2-	;2-	;1	*Sr22*
PI 573521	*T. m. a.*	Turkey	2-	2+;	2-	2	;1	*Sr22*
PI 596286	*T. m. a.*	Turkey	3/2-	3+	3+	4	;1/4	Het
PI 614650	*T. m. a.*	Ukraine	2-	2-	2-	2-	;1	*Sr22*
PI 614652	*T. m. a.*	Ukraine	2-	2-	2-	2-	;1	*Sr22*
CI 2433	*T. m. m.* [d]	Germany	3+	2+	3+	4	;1	*Sr21*
CI 13961	*T. m. m.*	United States	3+	3-2	3+	4	;1	*Sr21*
CI 13962	*T. m. m.*	United States	3+	3/;1	3+/;N	4	;1	Het
CI 13963	*T. m. m.*	United States	3+	2+	4	4	;1	*Sr21*
CI 13964	*T. m. m.*	United States	3+	3-	3+	4	;1	*Sr21*
CI 13965	*T. m. m.*	States	3+	2-2	3+	4	;1	*Sr21*
CI 14090	*T. m. m.*	Unknown	3+	3-	3/4	4	;1	*Sr21*
CI 14520	*T. m. m.*	Canada	3+	2	3	3+	;1	*Sr21*
CI 17652	*T. m. m.*	United States	3+	3-	4	4	;1	*Sr21*
CI 17653	*T. m. m.*	United States	3+	3	4	4	;1	*Sr21*
CI 17654	*T. m. m.*	United States	3+	3-	3+	4	;1	*Sr21*
CI 17655	*T. m. m.*	United States	3+	3-	4	4	;1	*Sr21*
CI 17657	*T. m. m.*	United States	3+	;	3+	4	0;	*Sr21*
CI 17658	*T. m. m.*	United States	3+	3	4	4	;1	*Sr21*
CI 17659	*T. m. m.*	United States	3+	3	4	4	;1	*Sr21*
CI 17660	*T. m. m.*	United States	3+	3	3/3+	4	;1	*Sr21*
CI 17661	*T. m. m.*	States	3	3+	3	4	;1	-
PI 94743	*T. m. m.*	Russia	3	2+3-	3/3+	4	;1	*Sr21*
PI 119422	*T. m. m.*	Turkey	3	3+	3+	4	3+	Sus.
PI 119423	*T. m. m.*	Turkey	3/3+	2-2	3+	4	;1	*Sr21*
PI 119435	*T. m. m.*	Turkey	3	2+3Z	3/3+	4	;1	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 167526	*T. m. m.*	Turkey	3+	4	3+	4	4	Sus.
PI 167589	*T. m. m.*	Turkey	3	3/2+	3	4	;1	*Sr21*
PI 167591	*T. m. m.*	Turkey	0/3	0/1/3	;/3+	3+	0;/4	*Sr21+ Sr35 Het*
PI 167611	*T. m. m.*	Turkey	3+/0	1	0/0;/3+	3+*	;1/0;	*Sr21+ Sr35 Het*
PI 167615	*T. m. m.*	Turkey	3+	;1/3-	3+	3+	;1/4	*Sr21 Het*
PI 167625	*T. m. m.*	Turkey	3	;/2	3+	3+	;1	*Sr21*
PI 167627	*T. m. m.*	Turkey	3/0	2+3-	3+/0	4/;2-	;1/0;	Het
PI 167634	*T. m. m.*	Turkey	3+	1	3+	4	;1	*Sr21*
PI 168803	*T. m. m.*	United States	3+	3-	4	4	;1	*Sr21*
PI 168804	*T. m. m.*	United States	3+	3+	4	4	;1	-
PI 168805	*T. m. m.*	United States	3+	12-	3/3N/3+	4	;1	*Sr21*
PI 168806	*T. m. m.*	States	3+	22+3Z	3+	4	;1	*Sr21*
PI 170196	*T. m. m.*	Turkey	3+	22+	3+	4	;1	*Sr21*
PI 190915	*T. m. m.*	Spain	4/3+	2-	4	3+	;1	*Sr21*
PI 190939	*T. m. m.*	Spain	3+/4	23Z	4	4	;1	*Sr21*
PI 190940	*T. m. m.*	Spain	3+	3-	4	4	;1	*Sr21*
PI 190942	*T. m. m.*	Spain	3+	1	3+	4	;1	*Sr21*
PI 190945	*T. m. m.*	Spain	1;	1	2-;	;1-	;1	*Sr22*
PI 190946	*T. m. m.*	Spain	3/3+	;1	3+	;2-	0;/;1	*Sr21+ Sr22*
PI 190947	*T. m. m.*	Spain	;1/3	;1	2-/3+	;1-	;1-	*Het*
PI 191094	*T. m. m.*	Spain	3+	3	3/3+	4	;1	*Sr21*
PI 191095	*T. m. m.*	Spain	4	3+	3	4	;1	-
PI 191096	*T. m. m.*	Spain	4/3	3+	3+	4	;1	-
PI 191097	*T. m. m.*	Spain	3+	33+	3+	4	;1	-
PI 191098	*T. m. m.*	Spain	3+	3+	3+	4	;1	-
PI 191146	*T. m. m.*	Spain	3+	3+	3+	4	;1	-
PI 191381	*T. m. m.*	Ethiopia	3+/0	0/;/;1	3+/0 0/3+	4	0;	*Sr21+ Sr35 Het*
PI 191383	*T. m. m.*	Ethiopia	0	0	LIF	4	;1	*Sr21+ Sr35*
PI 192063	*T. m. m.*	Portugal	3+	3+	3+	4	;1	-
PI 221329	*T. m. m.*	Yugoslavia	3+	3	3+	4	;1	-
PI 221393	*T. m. m.*	Yugoslavia	3+	2+	3+	4	;1	*Sr21*
PI 221413	*T. m. m.*	Yugoslavia	2+3	0;	2+3Z	2-2	0;	-
PI 221414	*T. m. m.*	Yugoslavia	2+3;/;1/ ;123Z	0	;123Z	0;	0;	-

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
								Sr21
PI 221415	*T. m. m.*	Yugoslavia	3+	3/2-	3+	4	;1	*Het*
PI 221416	*T. m. m.*	Yugoslavia	3+	3	3	4	4	Sus.
PI 225164	*T. m. m.*	Greece	3+	2	3+	4	;1	*Sr21*
PI 237659	*T. m. m.*	Kenya	3+	;1/2/3	3+	4	;1	*Sr21*
								Sr21
PI 254195	*T. m. m.*	Turkey	3+	3	-	4	4/;1	*Het*
					0/3+			
PI 264935	*T. m. m.*	Greece	0	0	LIF	4	4	*Sr35*
PI 265008	*T. m. m.*	Bosnia	3+	0	;123Z	;2-	0;	-
		United						
PI 266844	*T. m. m.*	Kingdom	3+	2+3	3+	4	;1	*Sr21*
PI 272535	*T. m. m.*	Hungary	3+	2+	3+	4	;1	*Sr21*
PI 272557	*T. m. m.*	Hungary	3+	4	4	4	4	Sus.
PI 272558	*T. m. m.*	Hungary	3+	4	4/3	4	4	Sus.
					2			
					LIF/3+			
					LIF/3+;			
PI 272560	*T. m. m.*	Hungary	0;	0	LIF	4	4	*Sr35*
PI 272561	*T. m. m.*	Hungary	2+3	;	3/3+	2-2	;	-
PI 272562	*T. m. m.*	Hungary	3	;/2	2+	;2-	;1	-
								Sr21+
PI 272563	*T. m. m.*	Hungary	3+	2+	3+	4/2-2	;1/;	*Het*
PI 277130	*T. m. m.*	Albania	3+	;	3+	2-2	0;	*Sr21*+
PI 277131	*T. m. m.*	Albania	3/2-	;	2/3+	2	;1/;	Het
PI 277133	*T. m. m.*	Albania	2/3	;	3	2-2	0;	Het
PI 277135	*T. m. m.*	Albania	3+	;	3/3+	2	0;	*Sr21*+
								Sr21+
PI 277136	*T. m. m.*	Albania	3+	;1-	3+/2	4	0;	*Het*
PI 277137	*T. m. m.*	Greece	0;	0	X- LIF	4	4	*Sr35*
PI 277138	*T. m. m.*	Germany	3	3/4	4	4	4	Sus.
PI 277140	*T. m. m.*	Germany	3+	3+	3/4	4	4	Sus.
PI 286068	*T. m. m.*	Poland	3+	;22+	3	4	;1	*Sr21*
		United						
PI 289599	*T. m. m.*	Kingdom	3+	2+3	4/3	4	;1	*Sr21*
		United						
PI 289605	*T. m. m.*	Kingdom	2-	2-	2-	;1	;1	*Sr22*
					3+/;3+			*Sr21*+
PI 290508	*T. m. m.*	Hungary	3+	;/2+	LIF	4	0;/;1	*Het*
PI 290509	*T. m. m.*	Hungary	3+	3-	3+	4	;1	*Sr21*
								Sr21+
PI 290511	*T. m. m.*	Hungary	3+	3-	3+	4/22+	;1	*Het*
PI 295058	*T. m. m.*	Bulgaria	3+	3-	3+	4	;1	*Sr21*
PI 306540	*T. m. m.*	Romania	;123Z	0;	;123Z	;1-	0	-
PI 306541	*T. m. m.*	Romania	3+	2-	3+	4	;1/0;	*Sr21*
PI 306542	*T. m. m.*	Romania	3	3	3	4	4	Sus.

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
								Sr21+
PI 306543	*T. m. m.*	Romania	0C	0	X- LIF	4	;1	*Sr35*
PI 306544	*T. m. m.*	Romania	;123+Z	0;	3+	;1-	0;	-
PI 306545	*T. m. m.*	Romania	3+	;1-	3	2-	0;	*Sr21*+
								Sr21+
PI 306546	*T. m. m.*	Romania	2+3/3+	;	3	2-2	0;	*Het*
PI 306547	*T. m. m.*	Romania	3+	;	3+	2-2	0;	*Sr21*+
PI 307984	*T. m. m.*	Morocco	4	22+	4	4	;1	*Sr21*
PI 323437	*T. m. m.*	Austria	3+	2+3-	4	4	;1	*Sr21*
PI 326317	*T. m. m.*	Azerbaijan	3	3-	3	;13-Z	;1/1+	*Sr21*+
PI 330550	*T. m. m.*	United Kingdom	2	2	2/2+	;1-	;1	*Sr22*
PI 330551	*T. m. m.*	United Kingdom	3+	3/2	4	4	;1	*Sr21*
PI 341413	*T. m. m.*	Turkey	3+	2-	3+	4	;1	*Sr21*
								Sr21+
					0/2-			*Sr35*
PI 343181	*T. m. m.*	Chile	0	0	/2++	4	4/0;	*Het*
PI 345133	*T. m. m.*	Yugoslavia	3+	;	3	4	;	*Sr21*
PI 345186	*T. m. m.*	Yugoslavia	4	;	3+	4	0;	*Sr21*
PI 345242	*T. m. m.*	Macedonia	3+	2-/3-	2++	3+	;1	*Sr21*+
PI 349049	*T. m. m.*	Armenia	3+	2-	3+	;13-Z	;1	*Sr21*+
PI 352473	*T. m. m.*	Italy	3+	2-/2+	3+	4	;1	*Sr21*
PI 352475	*T. m. m.*	Germany	3+	3+	4	4	4	Sus.
PI 352479	*T. m. m.*	Turkey	3+	;	2+3	3+	0	*Sr21*+
PI 352480	*T. m. m.*	Albania	;123+Z	0;	2+2++	;1-	0;	-
PI 352482	*T. m. m.*	Turkey	3+	12-	4	3+	;1	*Sr21*
PI 352483	*T. m. m.*	Spain	3+	1/2	3	4	;1	*Sr21*
PI 352484	*T. m. m.*	Balkans	3+	2	3+	4	;1	*Sr21*
PI 352486	*T. m. m.*	Switzerland	2/2+	2-	2/2+	2-	;1	*Sr22*
PI 355515	*T. m. m.*	Asia Minor	3+	2-2	3+	4	12	*Sr21*
								Sr22
PI 355516	*T. m. m.*	Asia Minor	3+/1;	2-/4	2+/4	2-/3	;1	*Het*
PI 355517	*T. m. m.*	Asia Minor	2	12-	2+	2-	;1	*Sr22*
PI 355519	*T. m. m.*	Iran	3+	23-	4	4	;1	*Sr21*
PI 355520	*T. m. m.*	Germany	4	1	4	4	0;	*Sr21*
PI 355521	*T. m. m.*	Asia Minor	2+3	2-/2+3	3	2-2	0;/1+	-
PI 355522	*T. m. m.*	Balkans	1;	;1	1;/2-	;12-	;1	*Sr22*
PI 355523	*T. m. m.*	Asia Minor	3+	3	4	3+	4	Sus.
PI 355524	*T. m. m.*	Germany	1;	;1	2-	;12-	;1	*Sr22*
PI 355526	*T. m. m.*	Belgium	4	3+	4	4	4	Sus.
PI 355528	*T. m. m.*	Asia Minor	3+	3	3	4	4	Sus.
PI 355529	*T. m. m.*	Belgium	4	3	4	4	;1+	*Sr21*
PI 355530	*T. m. m.*	Spain	4	2-/2+	4	3+	;1	*Sr21*
PI 355531	*T. m. m.*	Belgium	3+	2	3+	4	;1	*Sr21*
PI 355532	*T. m. m.*	Italy	4	3-	4	4	;1	*Sr21*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
								Sr21+
PI 355534	*T. m. m.*	Italy	0	0	X LIF	4	;1	*Sr35*
PI 355535	*T. m. m.*	Italy	3+	22+	3	;	;1-	*Sr21*+
								Sr21+
PI 355536	*T. m. m.*	Italy	0;	0	0;2-	0;	;1	*Sr35*+
PI 355537	*T. m. m.*	Turkey	3+	3+	3	4	4	Sus.
PI 355538	*T. m. m.*	Balkans	3+	;1-	3	4	;1-	*Sr21*
PI 355539	*T. m. m.*	Germany	4	;2-	3+	4	;1	*Sr21*
PI 355540	*T. m. m.*	Balkans	3+	;	2++	-	-	-
PI 355541	*T. m. m.*	Albania	2++;	0;	2++	0;	0;	-
PI 355543	*T. m. m.*	Germany	3+	3	3+	4	4	Sus.
PI 355544	*T. m. m.*	Germany	3+	2-/2+	3	3+	;1	*Sr21*
								Sr21
PI 355546	*T. m. m.*	Austria	3+	23-/3+	3+	3+	;1	*Het*
PI 355547	*T. m. m.*	Austria	3+	12-	3+	33+	;1	*Sr21*
PI 355548	*T. m. m.*	Austria	3+	12-	3+	;13Z	;1-	*Sr21*+
PI 355549	*T. m. m.*	Austria	4	2+3-	3+	3+	;1+	*Sr21*
		Switzerlan						*Sr21*
PI 355550	*T. m. m.*	d	3+	2+/3+	3+	3+	;1	*Het*
PI 362553	*T. m. m.*	Yugoslavia	2-	1	2-	;2=	;1	*Sr22*
PI 362554	*T. m. m.*	Yugoslavia	2-	;1	2-	;2-	;1	*Sr22*
PI 362610	*T. m. m.*	Macedonia	3/4	;1-	3	3+	0;	*Sr21*
PI 362616	*T. m. m.*	Macedonia	3/3+	;1-	3	3+	;	*Sr21*
PI 377648	*T. m. m.*	Yugoslavia	3+	;1	3	3+	0;	*Sr21*
PI 377662	*T. m. m.*	Yugoslavia	3+	;1	3	3+	0;	*Sr21*
PI 377666	*T. m. m.*	Yugoslavia	3/3+	;1	3	3+	0;	*Sr21*
PI 377667	*T. m. m.*	Yugoslavia	4	;	4	4	0;	*Sr21*
PI 377668	*T. m. m.*	Yugoslavia	4	;	3/4	4	0;	*Sr21*
PI 377669	*T. m. m.*	Yugoslavia	4	;1-	3	4	0;	*Sr21*
PI 377670	*T. m. m.*	Yugoslavia	4	;1	3	4	0;	*Sr21*
PI 377671	*T. m. m.*	Yugoslavia	3+/4	;1-/3	3+	4	0;	*Sr21*
PI 393496	*T. m. m.*	Israel	3+	3+	4	4	;1	-
PI 407640	*T. m. m.*	Turkey	3+	2+	4	4	;1	*Sr21*
								Sr22
PI 418582	*T. m. m.*	Azerbaijan	3+/1;	;1/4	4/2-	;1	;1	*Het*
PI 418583	*T. m. m.*	Georgia	4	3-	3+	4	;1	*Sr21*
PI 418587	*T. m. m.*	Russia	3+	2-	2+	33+	;1-	*Sr21*+
PI 427927	*T. m. m.*	Iraq	3+	22+/3	3	3+	;1	*Sr21*
PI 427959	*T. m. m.*	Iraq	3+	2	3	4	;1	*Sr21*
								Sr21+
PI 428149	*T. m. m.*	Sweden	3+	;	3+	4/;2-	0;	*Het*
PI 428150	*T. m. m.*	Romania	3+	2+/;	3+	33+	;1	*Sr21*
								Sr22
PI 428151	*T. m. m.*	Italy	2+	2-	2/2+	;1/3+	;1	*Het*
								Sr21+
								Sr35
PI 428152	*T. m. m.*	Bulgaria	0/3	0	X-	3+	;1	*Het*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
PI 428153	*T. m. m.*	United States	3	3	3+	33+	;1/1+2	*Sr21*
PI 428154	*T. m. m.*	Turkey	-	2+	3	3+	;1	*Sr21*
PI 428155	*T. m. m.*	United Kingdom	3	2N	3+	3+	;1	*Sr21*
PI 428156	*T. m. m.*	United Kingdom	3+	2+N	3+	3+	;1	*Sr21*
PI 428157	*T. m. m.*	United Kingdom	3+	1	4	4	;1	*Sr21*
PI 428158	*T. m. m.*	United Kingdom	3+	;12-	3+	;1-	;1	*Sr21*+
PI 428159	*T. m. m.*	United Kingdom	3+	;	3	;	0;	*Sr21*+
PI 428160	*T. m. m.*	Turkey	3+	1N	3+	3+	;1	*Sr21* *Sr35*
PI 428161	*T. m. m.*	Turkey	0/3+	0	3+ LIF	4	4	*Het*
PI 428162	*T. m. m.*	Turkey	3	2-	3+	3+	;1	*Sr21*
PI 428163	*T. m. m.*	Turkey	3	2	3	3+	;1	*Sr21* *Sr21*+
PI 428164	*T. m. m.*	Turkey	X--	0	X--	4	;1	*Sr35*
PI 428165	*T. m. m.*	Turkey	3+	0;	3	4	0;	*Sr21* *Sr35*
PI 428166	*T. m. m.*	Turkey	3+/0	3+/0	3+/2+ LIF/0	3+	3+	*Het* *Sr21*+ *Sr35*
PI 428167	*T. m. m.*	Turkey	0	0	2+/3+	3+	0;	*Het* *Sr21*
PI 428168	*T. m. m.*	Turkey	3+	2/3+	3	33+	;1/3+	*Het* *Sr21*+
PI 428169	*T. m. m.*	Turkey	;C	0	X-	3+	;1	*Sr35* *Sr21*+
PI 428170	*T. m. m.*	Turkey	0	0	X-	4	;1	*Sr35*
PI 428171	*T. m. m.*	Turkey	3+	2	3	33+	;1	*Sr21* *Sr21*+
PI 428172	*T. m. m.*	Turkey	3+	22+	3/2+	33+	;1	*Het*
PI 428173	*T. m. m.*	Turkey	2+3	3	3+	3+	4	-
PI 428174	*T. m. m.*	Turkey	3+	3-	3+	3+	;1/+	*Sr21* *Sr21*+
PI 428175	*T. m. m.*	Turkey	0;	0;	X--	33+	;1	*Sr35*
PI 428176	*T. m. m.*	Turkey	2+/3	22+/;1/3	2+/2+3 3+/;123	33+	;1/4	Het
PI 435000	*T. m. m.*	Yugoslavia	3+	0;	+Z	2	;	-
PI 435001	*T. m. m.*	Bosnia	3+	;	3+	2	;	*Sr21*+
PI 503874	*T. m. m.*	South Africa	3+	3+	3+	33+	;1	-
PI 518452	*T. m. m.*	Spain	3+	3+	3+	3+	;1	-
PI 538721	*T. m. m.*	Turkey	0;	0	X LIF	33+	4	*Sr35*

APPENDIX II continued

Accession	Species	Country	TRTTF	TTKSK	TTTTF	QFCSC	MCCFC	Gene Post.
								Sr21+ *Sr35*
PI 538722	*T. m. m.*	Turkey	0;	0/3+	X- LIF	3+	;1	*Het*
PI 542473	*T. m. m.*	United States	3	3	3	4	4	Sus.
PI 554525	*T. m. m.*	Turkey	1	2-	2-	;2-	;1-	*Sr22*
PI 554596	*T. m. m.*	Turkey	3+	;	3+	2+3-	0;	*Sr21*+
PI 560720	*T. m. m.*	Turkey	3+	2-	4	3+	4	-
PI 560723	*T. m. m.*	Turkey	3+/3	2-/3-	4	2	;1	*Sr21*+
PI 560725	*T. m. m.*	Turkey	3+	1/2+	2-/3-	4	;1	*Sr21*+
PI 560726	*T. m. m.*	Turkey	3+	2+3	3+	4	;1+	*Sr21*
PI 560727	*T. m. m.*	Turkey	3+	2	3+	4	1+	*Sr21*
PI 560728	*T. m. m.*	Turkey	3+	2+3	3+	3+	1+2	*Sr21*
PI 573523	*T. m. m.*	Turkey	2-	;N	2	;2-	;1-	*Sr22*
PI 573524	*T. m. m.*	Turkey	2+3	1	3+	;1	0;	-
PI 573525	*T. m. m.*	Turkey	3+	1	3+	22+	;1	*Sr21*+
PI 573526	*T. m. m.*	Turkey	3+	;	3+	2	0;	*Sr21*+
PI 573527	*T. m. m.*	Turkey	3+	2+/2-	4	4	;1	*Sr21*
PI 573528	*T. m. m.*	Turkey	2+/3	1/2+/23-Z/2+3-	4	4	;1	*Sr21*+ *Het* *Sr21*
PI 573529	*T. m. m.*	Turkey	3/3+	23Z/3+	3+	4	;1	*Het*
PI 584654	*T. m. m.*	Italy	3+	1/12-/3/3+	3/3+	4	3+	Het
PI 591871	*T. m. m.*	Georgia	3+	3-/3/3+	4	4	3	-
CI 17662	*T. m. m.*	United States	3+	3+	3+	4	12	-
PI 94740	*T. m. m.*	Spain	3+	3/2+3-	4/3+	3+	;1	*Sr21*

[a] Gene Postulation

[b] *Triticum monococcum* subsp. *aegilopoides*

[c] Susceptible

[d] *Triticum monococcum* subsp. *monococcum*

APPENDIX III: *Triticum monococcum* repeatability data

Accession	TRTTF rep. 1	TRTTF rep. 2	TTKSK rep. 1	TTKSK rep. 2	TTTTF rep. 1	TTTTF rep. 2
PI 352502	3/3+	3+	1	2-	3+	3
PI 401416	4	3+	2+	22+/2+3	4	3+
PI 427405	3+/4	3+	2+3Z	2+	3+/4	3
PI 427472	3+/4	4	1	1	3/3+	4
PI 427477	3+	4	12-Z	12-	4	3+
PI 427478	3+	3+	1/12Z	1/12Z	3+	3
PI 427481	3+	4	1/2+Z	1/12+	3+	3
PI 427491	3+/4	4	2+/12Z	12-/12Z	3+	4
PI 427507	3+	3+	3	2+	3+	3
PI 427511	3+	3+	1;	1	3+	3
PI 427537	3+	3/3+	1;	1	3+	3
PI 427538	3+	3+	2+3Z	12+Z/123Z	4	3
PI 427549	3+	4	3+	2+3/123Z	3+	3+
PI 427562	3+	4	3+	3+	3+	3
PI 427563	4	3+	3+	3	3+	3
PI 427564	4	4	3+	3+	3+/4	4
PI 427571	3+	3+	-	;1/1	4	4
PI 427575	3+	3	3	23Z	3+	4
PI 427578	4	4	23Z/3+	12+Z/123Z	4	4
PI 427603	3+/4	4	2+3Z	12+Z	3+	4
PI 427615	3+	3/2+	2+3Z	23Z	3+	4
PI 427616	3+/4	4	12+Z	12Z	3+	3
PI 427620	3+	4/3	3+	23Z/3+	4	4
PI 427637	4	4	3	123Z/23Z	3+	4
PI 427641	3+	3	12+Z	22+	3+/4	3
PI 427645	3+	3	12+Z	12Z	3+	3
PI 427646	4	3+/3	12+Z	;12-	3+	4
PI 427658	3+/4	3+	12+Z	12Z/23Z	4	4
PI 427668	3+	-	123Z	-	3+	3+
PI 427678	3+	3+	-	-	-	-
PI 427685	3+	3	12+Z	1;	3+	3
PI 427706	4	4	12Z	12	3+	3+
PI 427736	4	4	123Z	-	3+/4	3+
PI 427748	3+	4	12+Z	2-2	3+	3+
PI 427752	3+	4	23Z	2-3Z	3+/4	3+
PI 427757	3+	4	12	2-2Z	3+	3+
PI 427761	3+	4	12+Z	2-3Z	3+	4
PI 427770	4	4	3	3+	4	4
PI 427776	3+	-	2+3Z	3	3+	4
PI 427785	3+/4	4	12Z/123Z	12-	3+	4
PI 427787	3+	3+	2+3Z	2+3Z	3+	4
PI 427788	3+/4	4	123Z/12+Z	2+3Z	3+	4
PI 427789	4	4	23Z	2+3Z	3+	4
PI 427793	3+	3+	123Z	12/2+	3+	3+
PI 427807	3+/4	4/123+Z	1	1;/2+3Z/2+3+Z	3+	4
PI 427832	3+	4	123Z	22+Z	3+	3
PI 427843	4/3+	4	2+3Z	23Z	3+	3

APPENDIX III continued

Accession	TRTTF rep. 1	TRTTF rep. 2	TTKSK rep. 1	TTKSK rep. 2	TTTTF rep. 1	TTTTF rep. 2
PI 427849	4/3+	3	12+Z	2-	3+	3
PI 427850	4	4	12+Z	12+Z	3+	3+
PI 427851	4	4/3+	12+Z	12+Z	3+	3
PI 427854	-	-	-	-	3+	4
PI 427865	3+	4	23Z	23Z	3+/4	4
PI 427866	3+	3/3+	123Z	12+Z	3+	3/4
PI 427876	4	4	12+Z/123Z	12-Z	4	4
PI 427877	3+/4	4	12Z/12+Z	12+Z	4	4
PI 427913	4/3+	4	12-Z	12-	3+	4
PI 427928	-	-	-	-	-	-
PI 427929	3+	-	2+3Z	23Z	3+	4
PI 427933	3+	3+	12Z	2-2+Z	3+	3+
PI 427953	4	4	12+Z	2-2+Z	4/3+	4
PI 427963	3+	4	4	-	3+/4	-
PI 428010	4	4	23Z	23Z/2-3Z	3+	4
PI 503309	4	3+	12+/22+	23Z	3+	23Z/3+
PI 538524	3+	3	23Z	12+Z	3+	4/3
PI 538526	3+	4/3	3	2+3Z	3+	4
PI 538534	-	3+	2-	2-	3+	3+
PI 538537	3+	3	2-	12	3+	3+
PI 538545	4	4	11+	2-	3+/4	4
PI 538547	3+/4	4	2	2	4	3+
PI 538551	3+	4/3	2-	2-	4/3+	3+
PI 538566	-	3+	-	2-/2+	-	3
PI 538602	3+	3+	3+	2+3	3+	4
PI 538604	3+	4	2+3-	12+Z	3+	3+
PI 538619	4/3+	4	22+	2-2+	3+	3+
PI 554479	4	3+/4	3+/2+	3+	3+/4	4
PI 554480	3+	3+/3	3-	2+3Z	4	3
PI 554484	3+	3	2+/1	12Z/2-3Z	3+	3
PI 554485	3+	3+	2+	123Z	3+	3/4
PI 554494	3+	3	1;	-	3+	3+
PI 554495	3+/4	3	23-Z	12+Z	3+	3
PI 554497	3+	3	22+	2	4	3+
PI 554504	3+	3/3+	2+3Z	2+	4/3+	3
PI 554518	3+	3+	2+3-Z	2-2	4	3+
PI 554551	2-2	2-/;12-	2-	2-	2	2/2+
PI 554552	2-2	2-	;2-	;12-	22+	2
PI 554565	3+	-	3-	2	4	-
PI 560868	3+	3+	3-	2+3	3+	3
PI 170196	3+	3+	22+	2-2	4	3+
PI 190945	1	1;	1	1;	12-	2-;
PI 191098	4	3+	3+	2+3	4	3+
PI 221414	;1+3	2+3;/;1/;123Z	0	0;	X	;123Z
PI 277137	0	0;	0	0	4 LIF	X- LIF
PI 289605	1+2-2+	2-	2-	2-	2	2-
PI 290509	4	3+	3-	2+3	4	3+

APPENDIX III continued

Accession	TRTTF rep. 1	TRTTF rep. 2	TTKSK rep. 1	TTKSK rep. 2	TTTTF rep. 1	TTTTF rep. 2
PI 349049	3+	3+	2-	12+N	23+Z	3+
PI 352483	3+	3+	1/2	2-2	4	3
PI 355516	4/2/0;	3+/1;	2	2-	4	2+/4
PI 355537	3+	3+	3+	4	4	3
PI 362554	2-	2-	;1	1;	;12-	2-
PI 377670	3+	4	;1	;1-	3+	3
PI 428154	33+	-	2+	2-/2-2+	-	3
PI 428161	0	0/3+	0	0/2-2	X LIF	3+ LIF
PI 428162	3+	3	2-	12-2+;	3+	3+
PI 428164	0;/X--	X--	0	0	X- LIF	X--
PI 428170	0	0	0	0	X- LIF	X-
PI 542473	3+	3	3	3+	3+	3
PI 591871	3+	3+	3-/3/3+	;12Z/;123Z	;3+Z	4

APPENDIX IV: Seedling infection types of *T. aestivum* accessions to isolates of *Pgt*

Accession	BCCBC rep. 1	BCCBC rep. 2	MCCFC rep. 1	MCCFC rep. 2	QFCSC rep. 1	QFCSC rep. 2
CI 11649	1;	1N	2+;	32	-	2
CI 11781	;	;1	;1-	1+N	-	2
CI 11782	;	;	2	22+	-	2
CI 11783	;1	;1	2	2	-	2
CI 11945	;	;	2++	2+3	2	2
CI 12040	;	;	2++	2+3	3	3
CI 12044	;	0;	;	;	0;	0;
CI 12048	0;	0;	;1-	;1-	2-	2-
CI 12303	;1-	;	3;2+	3;2	2	2
CI 12324	;	;	3	3;2	2	2
CI 12355	0	;	;	;	2	2-
CI 12433	;1-	;	2+3	;13	2	2
CI 12499	;1-	;	3+	3	4	3
CI 12636	;1-	;	3+	3	2	2-
CI 12699	;1	;	0;	;	0;	0
CI 12737	;	;	;1-	;1-	2	2-
CI 12780	;	;	;	;1	2	2-
CI 12899	;	;	0	0;	0	0
CI 13100	;	;	0;	;	;	0;
CI 13204	0;	0	0	0;	0	0
CI 13407	0;	0;	0	0;	0	0
CI 13586	0;	0;	0;	;	0;	0
CI 13652	0;	0;	0;	;	0	0;
CI 13773	0;	0;	0;	0	0	0
CI 14142	0;	0;	0	0;	0;	0;
CI 14249	0;	0;	0	0;	0	0
CI 14267	0;	;	;	;	-	0;
CI 14275	;	0;	0;	0;	0	0
CI 14282	0;	0	0	0	0	0
CI 14334-1	2+	2+	3+	32+	22+	2++
CI 14334-2	2++	-	3+	3+	2++	2++
CI 14388	;	;	;1N	;1+N	0	;1
CI 14396	0;	0	0;	0	0	0

APPENDIX IV continued

Accession	BCCBC rep. 1	BCCBC rep. 2	MCCFC rep. 1	MCCFC rep. 2	QFCSC rep. 1	QFCSC rep. 2
CI 15533	0;	0	0;	0;	0;	0
CI 15536	0;	0	0	0;	0	0
CI 15544	;	;	0;	0	0	0
CI 15555	0;	0;	0	0	0	0
CI 15557	0	0	0	0	0	0
CI 15564	0;	0;	0	0;1	0	0
CI 15612	0	0	0	0	0	0
CI 15623	0	0	0	0	0	0
CI 15624	0	0	0	0	0	0
CI 15658	0	0	0	;	0	0
CI 15679	0	0;	0;1	;	0	;
CI 15680	-	;1	0;	;	0	0;
CI 15681	0;	0;	;1	1+N	0;	;
CI 15682	;1-	;	0	0;	;	-
CI 15685	0;	;	0	0;	0;	0
CI 15686	0;	0;	;	;	0;	0
CI 15711	0	0	0;	0	0	0
CI 15716	0	0	0;	0;	0	0
CI 15853	-	-	-	-	-	-
PI 185876	0;	;	0;	;	0	;
PI 199813	-	-	-	-	-	-
PI 234234	-	-	-	-	-	-
PI 234235	0	0	0	0	0	0
PI 234236	0	0	0	0	0	0
PI 234237	0;	0	0	0	0	0
PI 234238	0	0	-	0	0;	0;
PI 234239	0	;	0	0;	0	0;
PI 238391	0	0	;3-	;/;3-	0;3- LIF	0;
PI 254119	0	0	0;	;	0	0
PI 254121	0	0	-	;	0	0;
PI 254124	0;	0;	0	3-	2	2
PI 254126-2	0;	;	0/2-	1	-	;
PI 254137	0	0	0;	;	;1-	;1

APPENDIX IV continued

Accession	BCCBC rep. 1	BCCBC rep. 2	MCCFC rep. 1	MCCFC rep. 2	QFCSC rep. 1	QFCSC rep. 2
PI 254138	0	0	4	4	2+3-	3
PI 286545	;	;	0	2-	2	2
PI 286546	2	2+	-	2	2	2+
PI 297024	0	0;	0	0;	0	0
PI 299414	-	0;	0	0;	0	0
PI 323400	0	0	3+	0	0	0;
PI 410954	2	2	-	2	1;	2
PI 480270	0	0	0	0	0	0
PI 518648	;	;1-	0;	;1	0	0
PI 519501	0	0	;1	0	0	0
PI 519503	0	0;	0;	0;	0	0
PI 519553	0	0;	0;	0;	0	0;
PI 519623	;	;1	1N	1N	2	2N
PI 519681	0	0	0	;	0	0
PI 519711	0	0	0	0	0	0
PI 519720	2-	0;	0	0;	0	0;
PI 519805	0	-	0;	-	0;	-
PI 519943	0	0;	0	0;	0	0;
PI 520033	0;	-	0	-	0	-
PI 520093	0	0	0	0;	0	0
PI 520265	;	;	0	;1	0	0
PI 520373	2	2	;1-	;1	;1-	1;
LMPG-6	-	3	32	4	3-	4

APPENDIX IV continued

Accession	RCRSC rep. 1	RCRSC rep. 2	RKQQC rep. 1	RKQQC rep. 2	QTHJC rep. 1	QTHJC rep. 2
CI 11649	3	32;	3-	2N	-	2
CI 11781	3	23	1+	1N	-	2
CI 11782	-	2-	2	2	-	2
CI 11783	-	2	2	2	-	2
CI 11945	2	2+	22+;	1+C	2	2
CI 12040	3	3	3	3	2+	32
CI 12044	22+N	23N	2+	3-	2+	-
CI 12048	2	2	;1-	;	2-	2
CI 12303	2	2+3	2++	2+C	2	2
CI 12324	-	2+;	3	2+C	2	2
CI 12355	2	2	;1-	;1-	2	2
CI 12433	2	2	2++	2++	2	2
CI 12499	3+	4	4	4	4	4
CI 12636	2++	2++;	X-	X-	2	2
CI 12699	;1-	1;	;	1;	0;	0;
CI 12737	2	2	;1	;1-	2	2
CI 12780	2	2	2	2	2	2
CI 12899	2+	3-	-	2	-	0;
CI 13100	;11+C	;11+C	3	2+3	1N	1N
CI 13204	0;	0;	;1-	;1	1+ LIF	;
CI 13407	2-3	3	2	2+3-	0	2
CI 13586	0;	;	32+	2+3-	2	2+
CI 13652	0;	0;	2+;	0;/2+	0;	0;
CI 13773	0;	;1	0;	;11+	-	0;
CI 14142	0;	;	;	;	0	;
CI 14249	22+	22+	0	0;	0	0;
CI 14267	0	;	;	;	0	0;
CI 14275	0	0;	;11+	1+	2-	0;1+
CI 14282	0	0	3- LIF	3- LIF	0	0
CI 14334-1	2++2	3	2+	-	22+	22+
CI 14334-2	2++	3+	2+	-	2++	2++
CI 14388	;	11+C	;	;13-C	2+	2++
CI 14396	0;	;1	1+++;	;13	0;	0

APPENDIX IV continued

Accession	RCRSC rep. 1	RCRSC rep. 2	RKQQC rep. 1	RKQQC rep. 2	QTHJC rep. 1	QTHJC rep. 2
CI 15533	0; 1+++	0;1	0;	0;	0;	0;
CI 15536	LIF	1+++	0;	0;	0	0
CI 15544	3 LIF	3-	;1+	;1+	-	;11+
CI 15555	0	0	2+	2+	0;	;1 LIF
CI 15557	0	;11+	2+	3-	0	0
CI 15564	22+	2++	2+	13	0	0;
CI 15612	0	0	0;1	0	0	0;
CI 15623	0	0	0;	0;1	0	0;
CI 15624	0	0	0;	0;	;1	0
CI 15658	1+++	1+++	1++; LIF	;11+	0	0
CI 15679	2-	2-	2++	2++	2++	2++
CI 15680	2-	2-	2++	2++	-	2++
CI 15681	0;	0;	2++	2++	2++	3-
CI 15682	0	0;	2++	2++	2+	2+
CI 15685	;1	1	2++	2+3-	0	0
CI 15686	1	11+	32+	2++	2++	4
CI 15711	;1	;1	1++ LIF	2++	0;	0;
CI 15716	0;1	3-2	33-	3-	0	0
CI 15853	-	-	-	-	-	-
PI 185876	3+	3	1;	1+	;1	1+ LIF
PI 199813	-	-	-	-	-	-
PI 234234	-	-	-	-	-	-
PI 234235	3+	3+	4 LIF	3	0	0
PI 234236	4	4	-	4	0	0
PI 234237	-	4	4	4	0	0
PI 234238	2+3-	3	3+	3+	-	0
PI 234239	2+3-	2+3-	3+	3	0	0;
PI 238391	2+	2++	;1-	;	2	1++3-
PI 254119	22+	2++	22+	2++	;1	2++
PI 254121	;1+N	3	-	2++	32;	2++
PI 254124	42	3	22+	2++	2; LIF	2
PI 254126-2	1	1	-	2-	-	2++
PI 254137	1+N	1++	;11+N	;11+	-	3

APPENDIX IV continued

Accession	RCRSC rep. 1	RCRSC rep. 2	RKQQC rep. 1	RKQQC rep. 2	QTHJC rep. 1	QTHJC rep. 2
PI 254138	22+3	2++	;11+N	;11+N	4	4
PI 286545	2+3-	3-	-	3	2	2
PI 286546	2	2+	2	2	3-	3
PI 297024	0;1	2	3+ LIF	3	0	0;
PI 299414	-	0;	1+++	;1	;2	3-
PI 323400	3-2+	3	;13-	X-	0	0
PI 410954	2-	2	2-	2-	2	2
PI 480270	0	2-	-	3	0	0
PI 518648	0	0;	;1-	;1	2+ LIF	2++
PI 519501	0;	0;	1;	;11+	0	0;
PI 519503	;	0;	3-C	2+	0	;1+
PI 519553	;1	;1	0	2+;	0	0;
PI 519623	2-	2	2N	;11+	2++	3
PI 519681	;3	0;	0;	3	3	3-
PI 519711	0;	-	0;	;3	0	0
PI 519720	;1	;1	;3-	3;	0	0;
PI 519805	;1-	-	2	-	2	-
PI 519943	3-	2++C	0	4;1	0	0;
PI 520033	2	-	1+	1;	0	-
PI 520093	0;1	0;1	0	2	0	0
PI 520265	;	0;	2	2	2	2; LIF
PI 520373	1;	1	2	1	2	2
LMPG-6	3-	4	-	3+	4	3+

APPENDIX IV continued

Accession	TPMKC rep. 2[†]	TTTTF rep. 2	TTKSK rep. 1	TTKSK rep. 2	TTKSK rep. 3	TTKSK rep. 4
CI 11649	3;	31;	3	3	4/23	4
CI 11781	3;	31;	4	4	4	3+
CI 11782	3	4	;13	3/;	;13	-
CI 11783	22+	4	;1	4/0;	;1/;3/4	-
CI 11945	3	3	0/3	0/3	;3	0
CI 12040	3+	3	4	3+	4	3
CI 12044	3-;	4	X-	X-	X-	;2+
CI 12048	3	4	0;	0;	;3	0;
CI 12303	3	3+	0;	0;	;3N	;3
CI 12324	3+	2+	;3	0/;2/3	;3	0/3
CI 12355	3	4	;13	0;/3	;13	;3
CI 12433	3	3+	0	0	;3	;3
CI 12499	3	4	;3	;/3	;3	0;3
CI 12636	3	3+	;3	;	;3	0;1+
CI 12699	2-	2-	4	3+	4	1
CI 12737	3	3	0/1	0/1	;13	;3
CI 12780	3	3-	;3	0/3	;3	;3
CI 12899	;1	2;	X-N	3+/1N	3/X-N	;1/3-
CI 13100	;	3+	4	3+	4	3
CI 13204	;	1++	X+	-	X+	2/23-/;3
CI 13407	2-	2+3-	0	0	;1-	0;
CI 13586	;1	1+3	X-	-	X-	-
CI 13652	;3	0;	-	;	;12+	0;
CI 13773	;1+	0;	;	;	;11+	0;1
CI 14142	;	;1	;	;	;/X	;
CI 14249	;1	3	;12+	;1	;12+	0;
CI 14267	2-	11+	2-	2-	2+3	2N
CI 14275	13	1+++	;12	;	;12	;
CI 14282	0;	0;	0;	0/3	0;	0;
CI 14334-1	3	3	2+	2+	4	2++
CI 14334-2	3-	3+	4	-	-	;2
CI 14388	2+	1+++	-	3	3	3+
CI 14396	;1	3-	;1	;1	;1	;1

APPENDIX IV continued

Accession	TPMKC rep. 2[†]	TTTTF rep. 2	TTKSK rep. 1	TTKSK rep. 2	TTKSK rep. 3	TTKSK rep. 4
CI 15533	0;	0;	0;	0	0;	0;
CI 15536	0;	22++	;1	0	;1/3	0
CI 15544	;1	3	0;	0;	0;/4	23
CI 15555	0;	0;	;12-	0;1	;12-	;13
CI 15557	0;	3-	;	;1	;/;1	-
CI 15564	2++	3	;1	2+/;1	;1/3	-
CI 15612	0;	0;	;	0;1	;/;12-	0
CI 15623	0;	0;	;1	0;	;1	0
CI 15624	0;	0;1	;1	0;	;1	0;
CI 15658	;13-	2++	;	;	;/;12	-
CI 15679	2;	3	3	2+	3	3
CI 15680	2	11+	3	2++	3	3
CI 15681	2	;1	3	2+	3	4
CI 15682	;1+	0;	4	2	4	4
CI 15685	3	2+	0;	0;	0;/4	0;
CI 15686	2;	3	3+	2+C/;	3+	4
CI 15711	0;	3	0;1	23C/;1	0;1/3	0;
CI 15716	0;	3+	0;	;	0;	-
CI 15853	-	-	-	2	3	3
PI 185876	3-	3+	23-C	3-Feb	23-C	4
PI 199813	-	-	-	23	4	4
PI 234234	-	-	-	4	-	4
PI 234235	3-;	4	0;	0	0;	0;
PI 234236	4	4	0;	0	0;/3	0
PI 234237	3;	3+	0;	0	0;/4	0
PI 234238	3;	2++	0;	0;	0;	0
PI 234239	3;	2++	;	;	0;	0
PI 238391	3	3+	0;	0;	;1	0;
PI 254119	3+	3	X	0/3	X	3
PI 254121	;	3	0;	0	0;	0
PI 254124	3	3+	0	0	;1	0;1
PI 254126-2	2++	2+	0	0	;	0;
PI 254137	;	2	;2C	0	;2C	3

APPENDIX IV continued

Accession	TPMKC rep. 2†	TTTTF rep. 2	TTKSK rep. 1	TTKSK rep. 2	TTKSK rep. 3	TTKSK rep. 4
PI 254138	4	2+	;3-	0	;3-/4	;
PI 286545	3	3	4	0;2+	4	4
PI 286546	2	2	3+	3+	4	4
PI 297024	3	3	;1-	0;/2C	;1-	;
PI 299414	;	;1-	3-	2	3-	23
PI 323400	3-;	3-	0	0	0;	0
PI 410954	2	2	2-	0;	2-	2
PI 480270	;	3	;1-	0	;1-	0;
PI 518648	2	;1	3	-	3	4
PI 519501	0;	1+	0;	0	0;	0
PI 519503	3+	2	;1	0	;1/4	;3
PI 519553	;1	3	0;	0	0;	0
PI 519623	2++	3+	3	0/2+	3	31
PI 519681	;	-	3-	3-	4	3
PI 519711	0;	2+	0	0	0/4	0
PI 519720	3;	2++	-	0;	;1-	0
PI 519805	-	-	1	1	2-/2+	2-
PI 519943	3;	3+	0	0	0;	0
PI 520033	-	-	0;1	0;1	0;	0;
PI 520093	2	0;	0	0	0;	0
PI 520265	2	;	2-	0	2-/3	;
PI 520373	2+	2+	0	0	0;	3-
LMPG-6	3+	3-	3	3+	4	4

† The first replications of races TPMKC and TTTTF are displayed in Table 2.

APPENDIX V: Genotypic and phenotypic data used in constructing a linkage map of chromosome arm 6AL

Family	gwm169	wPt-8124	wPt-1695	wPt-1661	wmc580	gwm427	wPt-8764	wPt-8773
CSA	a [b]	a	a	a	a	a	d	d
TA4152-37	-	c	c	c	b	b	b	b
1	-	a	a	a	a	a	-	d
2	b	c	c	c	b	b	b	b
3	-	-	c	c	b	b	b	b
4	-	-	c	c	-	-	d	d
5	a	a	a	a	a	a	d	d
7	h	c	c	c	h	h	d	d
8	b	c	c	c	b	b	b	b
9	a	a	a	a	a	a	d	d
10	b	c	c	c	-	h	d	d
11	-	a	a	a	a	a	d	d
12	-	a	a	a	d	a	d	d
13	-	a	a	a	a	-	d	d
14	a	a	a	a	a	a	d	d
15	b	c	c	c	-	-	b	b
16	b	c	c	c	b	b	b	b
17	b	c	c	c	b	b	b	b
18	b	a	a	a	a	a	d	d
19	b	c	c	c	b	b	b	b
20	a	c	c	c	h	a	d	d
21	b	c	c	c	c	b	b	b
22	h	a	a	a	d	h	d	d
23	b	c	c	c	b	b	b	b
24	b	c	c	c	-	b	b	b
25	a	c	c	c	b	b	b	b
27	b	c	c	c	b	b	b	b
28	h	c	c	c	-	h	d	d
30	h	c	c	c	-	b	b	b
31	a	a	a	a	a	a	d	d
32	h	c	c	c	h	h	d	d
33	h	c	c	c	h	h	d	d
35	h	c	c	c	-	b	b	b
36	h	c	c	c	b	b	b	b
37	h	a	a	-	a	a	d	d
38	h	c	c	c	-	b	b	b
39	b	c	c	c	-	b	b	b
40	a	c	c	c	b	b	b	b
43	-	c	c	c	-	-	b	b
44	h	c	c	c	d	a	d	d
45	a	a	a	a	-	a	d	d

APPENDIX V continued.

Family	gwm169	wPt-8124	wPt-1695	wPt-1661	wmc580	gwm427	wPt-8764	wPt-8773
48	h	c	c	c	d	h	d	d
50	-	a	a	-	-	-	b	b
51	-	c	c	c	a	h	b	b
52	-	a	a	a	a	a	d	d
53	-	c	c	a	-	-	d	d
54	-	a	a	a	a	a	d	d
56	-	c	c	c	h	h	d	d
57	-	a	a	a	c	h	-	-
58	h	c	c	c	h	h	d	d
59	-	c	c	c	b	-	b	b
60	b	c	c	-	h	h	d	d
61	-	c	c	c	-	b	b	b
62	-	a	a	c	-	-	b	b
63	-	-	-	-	-	-	-	-
65	b	-	-	c	h	h	-	-
67	h	c	c	c	-	h	-	d
70	h	c	c	c	h	h	d	d
72	b	c	c	c	-	b	b	b
73	a	a	a	c	h	-	d	d
74	b	c	c	c	b	b	b	b
75	a	a	a	a	a	a	d	d
77	h	c	c	c	h	h	d	d
78	b	c	c	c	b	b	b	b
80	b	c	c	c	h	h	d	d
81	-	c	c	c	b	-	b	b
82	a	a	a	a	a	a	d	d
84	-	a	a	c	h	-	-	-
85	b	c	c	c	b	b	b	b
87	-	a	a	a	a	a	d	d
88	-	c	c	c	a	-	-	-
89	-	c	c	c	-	-	b	b
90	a	c	c	c	h	h	d	d
91	h	-	c	c	h	h	d	d
92	h	c	c	c	d	h	-	d
93	h	c	c	c	-	-	d	d
95	b	c	c	c	b	b	b	b
96	b	-	c	-	b	b	b	b
98	-	c	c	a	-	b	b	b
99	b	c	c	c	b	b	b	b
100	h	-	c	c	-	h	d	d
101	h	c	c	c	b	b	b	b
102	b	c	c	c	-	h	d	d
103	b	c	-	c	h	h	d	d

APPENDIX V continued.

Family	gwm169	wPt-8124	wPt-1695	wPt-1661	wmc580	gwm427	wPt-8764	wPt-8773
105	-	c	c	-	a	-	d	d
106	h	c	c	c	b	-	b	b
108	h	-	-	c	h	h	-	-
111	b	c	c	c	b	b	b	b
113	h	c	c	c	h	h	d	d
114	b	a	a	a	a	a	d	d
115	h	-	-	c	h	h	-	-
116	h	a	a	a	a	a	d	d
117	h	-	-	c	h	h	d	d
118	-	-	-	-	-	-	-	-
119	h	-	-	-	h	h	-	-
120	h	-	-	c	h	-	d	d

APPENDIX V continued.

Family	TTTTF	TTKSK [a]	wPt-5696	wPt-2216	wPt-3247	wPt-7204	wPt-9976	barc104
CSA	a	a	d	d	d	d	d	a
TA4152-37	b	b	b	b	b	b	b	b
1	a	a	-	d	d	d	d	a
2	b	b	b	b	b	b	b	b
3	b	b	b	b	b	b	d	-
4	h	b	d	d	d	d	d	-
5	a	a	d	d	d	d	d	h
7	h	h	d	d	d	d	-	h
8	b	b	b	b	b	b	-	b
9	a	a	d	d	d	d	d	h
10	h	h	d	d	-	d	-	h
11	h	h	d	d	d	d	d	h
12	a	a	d	d	d	d	d	h
13	a	b	d	d	d	d	d	h
14	a	h	d	d	d	d	d	a
15	b	b	b	b	b	b	b	b
16	b	b	b	b	b	b	b	b
17	b	b	b	b	b	b	b	b
18	a	a	d	d	d	d	d	a
19	b	b	b	b	b	b	b	b
20	h	h	d	d	-	d	d	h
21	b	b	b	b	b	b	b	b
22	a	a	d	d	d	d	d	h
23	-	b	b	b	b	b	b	b
24	b	b	b	b	b	b	b	b
25	b	b	b	b	b	b	b	-
27	-	h	b	b	b	b	b	b
28	h	h	d	d	d	d	-	a
30	h	h	d	d	-	d	-	a
31	a	h	d	d	d	d	d	h
32	h	h	d	d	d	d	d	h
33	h	a	d	d	d	d	d	h
35	-	-	b	b	b	b	b	b
36	-	b	b	b	b	b	b	b
37	a	h	d	d	d	d	d	h
38	b	b	b	b	b	b	b	b
39	b	b	b	b	b	b	b	-
40	b	b	b	b	b	b	b	b
43	b	b	b	b	b	b	b	h
44	h	h	-	d	d	d	d	h
45	a	h	d	d	d	d	d	h

APPENDIX V continued.

Family	TTTTF	TTKSK [a]	wPt-5696	wPt-2216	wPt-3247	wPt-7204	wPt-9976	barc104
48	h	h	d	d	d	d	-	a
50	a	b	b	d	d	d	d	-
51	h	h	-	d	-	d	d	h
52	a	h	d	d	d	d	d	a
53	a	h	d	d	d	d	d	-
54	-	h	d	d	d	d	-	h
56	b	b	d	d	d	d	d	h
57	a	h	d	d	d	d	d	h
58	b	b	b	b	b	b	b	b
59	b	b	b	b	b	b	b	-
60	h	h	d	d	d	d	d	a
61	b	b	b	b	b	b	b	b
62	h	h	d	b	d	d	d	a
63	b	b	-	-	-	-	-	-
65	b	b	d	d	d	d	d	h
67	h	b	d	d	d	d	d	a
70	h	h	d	d	d	d	-	c
72	b	b	b	b	b	b	b	b
73	h	h	-	d	d	d	d	h
74	b	b	b	b	b	b	b	b
75	a	h	d	d	d	d	d	h
77	h	h	d	d	d	d	d	h
78	b	b	b	b	b	b	b	b
80	h	h	d	d	d	b	d	a
81	b	h	b	b	b	b	b	b
82	a	h	d	d	d	d	d	a
84	h	h	-	d	d	d	d	h
85	b	b	b	b	b	b	b	-
87	a	a	d	d	d	d	d	h
88	h	h	d	-	-	d	d	h
89	h	h	b	b	d	d	d	c
90	h	h	d	-	d	d	d	h
91	h	h	d	d	d	d	d	h
92	h	h	d	d	d	-	d	h
93	h	h	d	d	-	-	d	h
95	b	b	b	b	b	b	b	b
96	h	h	d	d	-	d	d	a
98	h	h	d	d	d	d	-	c
99	b	b	b	b	b	b	b	-
100	h	h	d	d	d	d	-	a
101	b	b	b	b	b	b	b	b
102	h	h	d	d	d	d	d	h
103	h	h	d	d	-	d	d	h

APPENDIX V continued.

Family	TTTTF	TTKSK [a]	wPt-5696	wPt-2216	wPt-3247	wPt-7204	wPt-9976	barc104
105	h	h	d	d	-	d	d	h
106	b	b	b	b	b	b	b	b
108	h	h	d	d	d	d	d	h
111	b	h	b	b	b	b	b	b
113	h	h	d	d	d	d	-	a
114	a	a	d	d	d	d	d	h
115	h	h	b	d	d	d	d	h
116	a	h	d	d	d	d	d	h
117	h	h	d	d	-	d	d	h
118	b	b	-	-	-	-	-	-
119	h	h	-	-	-	-	-	h
120	h	h	d	d	d	d	d	a

[a] TTKSK phenotypic data was not used in mapping

[b] 'a' indicates Chinese Spring (CSA) parental type, 'b' indicates TA 4152-37 parental type, 'c' indicates heterozygous/heterogeneous or TA 4152-37 parental type, 'd' indicates heterozygous/heterogeneous or Chinese Spring parental type, and 'h' indicates heterozygous (genotypic marker) or heterogeneous (phenotypic marker).

APPENDIX VI: Summary of genotypic and phenotypic data used in constructing linkage map on chromosome arm 2BL

F.[a]	gwm 319	gwm 388	wPt-4199	wPt-3109	wmc 175	wPt-1140	barc 101	gwm 120	gwm 47	wPt-3132	R[d]	wPt-8460	wmc 332
56[b]	a[c]	a	a	d	a	d	a	a	a	d	a	a	a
CS	b	b	c	b	-	b	b	b	c	b	b	c	b
5	h	h	c	-	c	-	h	h	-	-	h	c	h
7	b	b	-	d	c	d	h	h	c	d	h	-	h
8	h	h	c	d	c	-	h	h	c	d	h	-	h
9	b	b	c	b	c	b	b	b	c	d	h	c	h
11	a	a	a	d	a	d	a	a	a	d	a	a	a
12	a	a	a	d	a	d	a	a	a	d	a	a	a
14	a	a	a	d	a	d	a	a	a	d	a	c	h
15	h	h	a	d	c	d	h	h	c	d	a	a	h
18	h	h	c	b	c	d	h	h	a	d	a	a	h
21	h	h	-	-	a	-	-	a	a	-	a	-	a
28	h	h	c	d	c	d	h	h	c	d	h	c	h
31	a	a	a	d	a	d	a	a	a	d	a	a	a
33	b	b	c	b	c	b	b	b	c	b	b	c	h
34	a	a	a	d	a	d	a	a	a	d	a	a	a
36	b	b	c	b	c	b	b	b	c	b	b	c	b
37	h	h	c	-	c	d	h	h	c	d	h	-	h
39	b	b	c	b	c	-	b	b	-	b	b	c	b
40	h	a	a	d	c	d	a	h	a	d	a	a	h
41	b	b	c	b	c	b	b	b	c	-	h	c	h
42	h	h	c	d	c	d	h	h	a	d	a	c	b
43	h	h	c	d	c	d	h	b	c	-	h	-	a
45	-	a	a	d	a	d	a	a	a	d	a	a	a
47	h	h	c	d	c	d	h	h	c	d	h	c	h
49	a	a	c	d	c	d	h	h	c	d	h	c	h
50	h	h	c	-	c	d	h	h	c	d	h	c	h
51	h	h	-	-	a	-	a	a	a	-	a	-	a
55	h	h	c	-	c	d	b	b	c	d	h	c	h
58	h	h	c	b	c	b	b	b	c	b	b	c	h
59	h	h	-	d	c	d	h	h	c	-	h	c	h
60	h	b	c	b	c	b	b	b	c	b	b	c	a
61	b	h	c	d	c	-	c	h	c	d	h	c	h
63	a	h	c	d	c	d	h	h	c	d	h	c	h
64	d	h	a	-	c	d	h	h	c	-	h	c	h
65	a	a	a	-	a	-	a	a	a	d	a	a	a
66	b	b	c	b	c	b	b	b	c	d	h	-	h
67	h	h	c	d	c	d	h	h	c	d	h	a	h
68	a	a	a	d	a	d	a	a	a	d	a	a	a
69	h	c	c	b	c	b	b	b	c	b	b	c	b
70	b	b	c	b	c	b	b	b	c	b	b	c	b

APPENDIX VI continued.

F.[a]	gwm 319	gwm 388	wPt-4199	wPt-3109	wmc 175	wPt-1140	barc 101	gwm 120	gwm 47	wPt-3132	R [d]	wPt-8460	wmc 332
71	h	c	c	b	c	b	b	b	c	b	b	c	b
72	h	h	c	-	c	d	h	h	c	d	h	c	-
73	d	h	c	d	c	d	h	h	c	-	h	c	h
74	a	c	-	-	c	-	b	b	c	-	c	-	b
75	a	h	c	d	c	d	h	h	c	-	h	c	h
76	h	a	-	-	c	-	h	h	c	-	b	-	b
78	h	h	-	-	c	-	h	h	c	-	h	-	h
79	b	c	-	-	c	-	b	b	c	-	b	-	b
80	a	a	c	b	a	d	a	a	a	d	a	a	h
82	a	a	a	-	a	d	-	a	a	d	a	-	a
83	b	c	c	b	c	b	b	b	c	b	b	c	b
84	a	a	a	d	a	d	a	a	a	d	a	a	a
85	d	h	c	d	c	d	h	h	c	-	a	c	h
87	b	a	-	-	a	-	a	a	a	-	a	-	a
88	b	c	-	-	c	-	b	b	c	-	b	-	b
89	h	b	c	b	a	b	b	b	c	b	b	c	b
90	h	h	-	d	c	-	h	h	c	d	h	c	a
91	h	h	-	-	c	-	h	h	c	-	h	-	a
92	a	h	-	-	c	-	h	h	c	-	h	-	h
93	b	c	c	b	c	b	b	b	c	b	b	c	b
94	d	h	-	d	c	d	h	h	c	d	h	c	h
95	d	h	a	d	c	d	h	h	c	d	d	c	h
96	h	h	c	d	c	d	h	h	a	d	a	a	a
97	d	h	c	d	c	d	h	h	c	d	h	c	h
98	h	h	c	-	c	d	h	h	c	d	h	c	h
99	a	a	a	d	a	d	a	a	a	d	a	a	a
100	h	h	-	-	c	-	h	h	c	-	b	-	h
101	h	-	-	-	c	-	b	b	c	-	b	-	b
102	h	h	-	d	c	d	h	h	c	d	h	c	h
103	h	h	c	-	c	d	h	h	c	d	h	c	b
104	h	h	-	-	c	-	h	h	c	-	h	-	h
105	a	a	a	d	a	d	a	a	a	d	a	a	a
106	a	h	c	d	c	d	h	h	c	d	h	c	h
107	h	c	c	d	c	d	h	h	c	-	h	c	h
109	a	a	a	d	a	d	a	a	a	d	a	a	h
110	c	h	c	b	c	b	b	b	c	b	b	c	h
111	a	h	c	-	c	d	h	h	c	-	h	c	h
112	a	a	-	-	a	-	h	h	c	-	h	-	a
113	h	h	-	-	a	-	h	h	c	-	h	-	h
114	a	a	a	d	a	d	a	a	a	d	a	a	b
115	a	a	a	d	a	d	a	a	a	d	a	a	h

[a] Family

[b] Gabo 56

[c] 'a' indicates CI 14035 parental type, 'b' indicates Chinese Spring (CSA) parental type, 'c' indicates heterozygous/heterogeneous or Chinese Spring parental type, 'd' indicates heterozygous/heterogeneous or CI 14035 parental type, and 'h' indicates heterozygous (genotypic marker) or heterogeneous (phenotypic marker).

[d] 'R' indicates resistance to TTKSK.

APPENDIX VII: Summary of F_2 genotypic and $F_{2:3}$ phenotypic data used in constructing linkage map with *Sr28* on chromosome arm 2BL

Family	wmc332	*Sr28*	wPt-7004	wPt-5128	wPt-7161
LMPG-6	b[a]	b	c	c	c
SD 1691	a	a	a	a	a
1	h	c	c	a	c
3	h	h	c	c	c
4	h	h	c	-	-
5	h	h	c	c	c
6	b	b	c	c	c
7	h	b	c	c	c
8	h	h	-	c	c
10	b	b	c	c	c
11	b	h	c	c	c
12	c	b	c	c	c
13	h	h	c	c	a
14	c	b	c	c	c
15	h	b	c	c	c
16	b	b	c	c	c
19	h	h	c	c	-
20	b	b	c	-	c
21	b	b	c	c	c
22	h	h	c	c	c
23	h	c	c	c	c
24	b	b	c	-	c
25	b	a	c	c	c
26	b	b	c	c	c
28	b	b	c	-	c
29	h	h	c	c	c
30	b	b	c	c	c
31	b	b	c	c	c
32	h	h	c	c	-
33	h	h	c	c	c
34	a	a	a	a	a
35	h	h	c	c	-
36	a	a	a	a	a
37	a	a	a	a	a
38	a	a	a	a	a
39	h	-	a	a	a
41	h	h	c	c	c
42	h	a	a	a	a
43	h	h	c	c	c
44	h	h	c	c	c
45	h	h	c	c	c
46	-	h	c	c	c

APPENDIX VII continued.

Family	wmc332	*Sr28*	wPt-7004	wPt-5128	wPt-7161
47	b	h	c	c	c
48	-	h	c	-	c
49	a	a	a	a	a
50	h	c	c	c	c
51	-	a	a	a	a
52	h	h	c	c	c
53	h	h	c	c	c
54		a	a	a	a
56	a	a	a	a	a
57	-	a	a	a	a
58	h	h	c	c	c
59	a	a	a	a	a
55	a	a	a	a	a
60	h	h	-	-	-
62	a	a	a	a	a
63	a	a	a	a	a
64	h	h	c	c	c
65	a	a	a	a	-
66	-	a	a	a	-
67	-	h	c	c	c
68	-	a	a	a	a
69	h	h	c	c	c
70	-	h	-	c	c
71	h	h	-	c	c
72	h	h	c	c	c
74	h	c	c	c	-
75	-	h	c	a	-
76	b	c	c	c	c
77	a	h	c	c	c
79	h	h	-	c	c
80	h	h	c	c	c
82	h	h	c	c	c
83	h	c	c	c	a
84	h	h	c	c	c
85	h	h	c	c	c
86	h	h	c	c	c
87	d	h	c	c	c
88	h	h	-	-	-
89	h	h	-	-	-
90	h	c	c	c	c
91	-	c	c	c	c
92	a	h	c	c	c
93	h	h	c	c	c
94	h	h	c	c	c

APPENDIX VII continued.

Family	wmc332	*Sr28*	wPt-7004	wPt-5128	wPt-7161
95	h	h	c	c	c
96	d	a	a	a	a
97	b	h	c	c	c
98	h	h	c	c	c
99	h	h	c	c	c
101	h	h	c	c	c
102	h	-	c	c	c
103	a	h	a	a	a
104	h	-	c	c	c
105	h	c	c	c	-

[a] 'a' indicates SD 1691 parental type, 'b' indicates LMPG-6 parental type, 'c' indicates heterozygous/heterogeneous or LMPG-6 parental type, 'd' indicates heterozygous/heterogeneous or SD 1691 parental type, and 'h' indicates heterozygous (genotypic marker) or heterogeneous (phenotypic marker).